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(54) Title: NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

(57) Abstract: Nucleotide sequences are isolated from *Arabidopsis thaliana* that code for proteins essential for plant growth and development. The essentially of the proteins may be exploited by recombinantly expressing the proteins and using them in screening assays to identify compounds that interact with or inhibit the proteins and are therefore potential herbicides.

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## NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

The present invention pertains to nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. The invention particularly relates to methods of using these proteins as herbicide targets, based on this essentiality.

The use of herbicides to control undesirable vegetation such as weeds in crop fields has become almost a universal practice. The herbicide market exceeds 15 billion dollars annually. Despite this extensive use, weed control remains a significant and costly problem for farmers.

Effective use of herbicides requires sound management. For instance, the time and method of application and stage of weed plant development are critical to achieving good weed control with herbicides. Because various weed species are resistant to herbicides, the production of effective new herbicides becomes increasingly important. New herbicides can now be discovered using high-throughput screens that implement recombinant DNA technology. Metabolic enzymes found to be essential to plant growth and development can be recombinantly produced through standard molecular biological techniques and utilized as herbicide targets in screens for novel inhibitors of the enzyme activity. More generally, any essential plant protein can be used to screen for inhibitors of its activity. The novel inhibitors discovered through such screens may then be used as herbicides to control undesirable vegetation.

In view of the above, there remain persistent and ongoing problems with unwanted or detrimental vegetation growth (e.g. weeds). Furthermore, as the population continues to grow, there will be increasing food shortages. Therefore, there exists a long felt, yet unfulfilled need, to find new, effective, and economic herbicides.

In view of these needs, it is an object of the invention to provide nucleic acid molecules from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. It is another object to provide the essential proteins encoded by these essential nucleotide sequences for assay development to identify

inhibitory compounds with herbicidal activity. It is still another object of the present invention to provide an effective and beneficial method for identifying new or improved herbicides using the essential proteins of the invention.

In furtherance of these and other objects, the present invention provides nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant viability. Genetic results show that when any of the nucleotide sequences of the invention are mutated in *Arabidopsis thaliana*, the resulting phenotype is embryo or seedling lethal in the homozygous state. In particular, by using *Ac/Ds* transposon or T-DNA-mediated mutagenesis, the inventors of the present invention are the first to demonstrate that the activity of each protein of the present invention is essential for plant growth in *Arabidopsis thaliana*.

This knowledge is exploited to provide novel herbicide modes of action. The critical role in plant growth of the proteins encoded by each of the nucleotide sequences of the invention implies that chemicals that inhibit the function of any one of these proteins in plants are likely to have detrimental effects on plants and are potentially good herbicide candidates. Thus, the proteins encoded by the essential nucleotide sequences provide the bases for assays designed to easily and rapidly identify novel herbicides.

The present invention therefore provides methods of using a purified protein encoded by any one of the nucleotide sequences described below to identify inhibitors thereof, which can then be used as herbicides to suppress the growth of undesirable vegetation, *e.g.* in fields where crops are grown, particularly agronomically important crops such as maize and other cereal crops such as wheat, oats, rye, sorghum, rice, barley, millet, turf and forage grasses, and the like, as well as cotton, sugar cane, sugar beet, oilseed rape, and soybeans.

Disclosed herein are nucleic acid molecules isolated from *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence, the complement of which hybridizes under stringent conditions to a sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-95. In another embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

The present invention also provides a chimeric construct comprising a promoter operatively linked to a nucleic acid molecule according to the present invention, wherein the promoter is preferably functional in a eukaryote, wherein the promoter is preferably heterologous to the nucleic acid molecule. The present invention further provides a recombinant vector comprising a chimeric construct according to the present invention, wherein said vector is capable of being stably transformed into a host cell. The present invention still further provides a host cell comprising a nucleic acid molecule according to the present invention, wherein said nucleic acid molecule is preferably expressible in the cell. The host cell is preferably selected from the group consisting of a plant cell, a yeast cell, an insect cell, and a prokaryotic cell. The present invention additionally provides a plant or seed comprising a plant cell according to the present invention.

The present invention also provides proteins essential for plant growth in *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. In accordance with another embodiment, the present invention also relates to the recombinant production of proteins of the invention and methods of using the proteins of the invention in assays for identifying compounds that interact with the protein.

According to another aspect, the present invention provides a method of identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind to said polypeptide, under conditions conducive to binding; (b) selecting a compound identified in (a) that binds to said polypeptide; (c) applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID



NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

According to yet another aspect, the present invention provides a method of  
5 identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit the activity of said polypeptide, under conditions conducive to inhibition; (b) selecting a compound identified in (a) that inhibits the activity of said polypeptide; (c)  
10 applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid sequence at least 99% identical to an amino acid  
15 sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

20 The present invention still further provides a method for killing or inhibiting the growth or viability of a plant, comprising inhibiting expression in said plant of a protein having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

25 Other objects and advantages of the present invention will become apparent to those skilled in the art and from a study of the following description of the invention and non-limiting examples. The entire contents of all publications mentioned herein are hereby incorporated by reference.

### 30 BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

Odd numbered SEQ ID NOs:1-95 are nucleotide sequences isolated from *Arabidopsis thaliana* that are more fully described in Table 5 below.

Even numbered SEQ ID NOs:2-96 are protein sequences encoded by the immediately preceding nucleotide sequence, *e.g.*, SEQ ID NO:2 is the protein encoded by the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:4 is the protein encoded by the nucleotide sequence of SEQ ID NO:3, etc.

5 SEQ ID NOs:101-125 are PCR primers.

## DEFINITIONS

For clarity, certain terms used in the specification are defined and presented as follows:

10 "Associated with / operatively linked" refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

15 A "chimeric construct" is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulatory nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulatory nucleic acid sequence of the chimeric construct is not normally  
20 operatively linked to the associated nucleic acid sequence as found in nature.

Co-factor: natural reactant, such as an organic molecule or a metal ion, required in an enzyme-catalyzed reaction. A co-factor is *e.g.* NAD(P), riboflavin (including FAD and FMN), folate, molybdopterin, thiamin, biotin, lipoic acid, pantothenic acid and coenzyme A, S-adenosylmethionine, pyridoxal phosphate, ubiquinone, menaquinone. Optionally, a co-factor  
25 can be regenerated and reused.

A "coding sequence" is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

30 Complementary: "complementary" refers to two nucleotide sequences that comprise antiparallel nucleotide sequences capable of pairing with one another upon formation of hydrogen bonds between the complementary base residues in the antiparallel nucleotide sequences.

Enzyme activity: means herein the ability of an enzyme to catalyze the conversion of a substrate into a product. A substrate for the enzyme comprises the natural substrate of the enzyme but also comprises analogues of the natural substrate, which can also be converted, by the enzyme into a product or into an analogue of a product. The activity of the enzyme is measured for example by determining the amount of product in the reaction after a certain period of time, or by determining the amount of substrate remaining in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of an unused co-factor of the reaction remaining in the reaction mixture after a certain period of time or by determining the amount of used co-factor in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of a donor of free energy or energy-rich molecule (*e.g.* ATP, phosphoenolpyruvate, acetyl phosphate or phosphocreatine) remaining in the reaction mixture after a certain period of time or by determining the amount of a used donor of free energy or energy-rich molecule (*e.g.* ADP, pyruvate, acetate or creatine) in the reaction mixture after a certain period of time.

Essential: an "essential" *Arabidopsis thaliana* nucleotide sequence is a nucleotide sequence encoding a protein such as *e.g.* a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein that is essential to the growth or survival of the plant.

Expression Cassette: "Expression cassette" as used herein means a nucleic acid molecule capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operatively linked to the nucleotide sequence of interest which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, *i.e.*, the particular DNA sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of

the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter that initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as a plant, the promoter can also be specific to a particular tissue or organ or stage of development.

Gene: the term "gene" is used broadly to refer to any segment of DNA associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

Heterologous/exogenous: The terms "heterologous" and "exogenous" when used herein to refer to a nucleic acid sequence (*e.g.* a DNA sequence) or a gene, refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" nucleic acid (*e.g.* DNA) sequence is a nucleic acid (*e.g.* DNA) sequence naturally associated with a host cell into which it is introduced.

Hybridization: The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

Inhibitor: a chemical substance that inactivates the enzymatic activity of a protein such as a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein. The term "herbicide" (or "herbicidal compound") is used herein to define an inhibitor applied to a plant at any stage of development, whereby the herbicide inhibits the  
5 growth of the plant or kills the plant.

Interaction: quality or state of mutual action such that the effectiveness or toxicity of one protein or compound on another protein is inhibitory (antagonists) or enhancing (agonists).

A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when  
10 the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

Isogenic: plants that are genetically identical, except that they may differ by the presence or absence of a heterologous DNA sequence.

Isolated: in the context of the present invention, an isolated DNA molecule or an  
15 isolated enzyme is a DNA molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, in a transgenic host cell.

Mature protein: protein from which the transit peptide, signal peptide, and/or  
20 propeptide portions have been removed.

Minimal Promoter: the smallest piece of a promoter, such as a TATA element, that can support any transcription. A minimal promoter typically has greatly reduced promoter activity in the absence of upstream activation. In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription.

25 Modified Enzyme Activity: enzyme activity different from that which naturally occurs in a plant (*i.e.* enzyme activity that occurs naturally in the absence of direct or indirect manipulation of such activity by man), which is tolerant to inhibitors that inhibit the naturally occurring enzyme activity.

Native: refers to a gene that is present in the genome of an untransformed plant cell.

30 Naturally occurring: the term "naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be

isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

Nucleic acid: the term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.* degenerate codon substitutions) and complementary sequences and as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.* 19: 5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260: 2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8: 91-98 (1994)). The terms "nucleic acid" or "nucleic acid sequence" may also be used interchangeably with gene, cDNA, and mRNA encoded by a gene.

"ORF" means open reading frame.

Percent identity: the phrases "percent identical" or "percent identical," in the context of two nucleic acid or protein sequences, refers to two or more sequences or subsequences that have for example 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably at least 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Preferably, the percent identity exists over a region of the sequences that is at least about 50 residues in length, more preferably over a region of at least about 100 residues, and most preferably the percent identity exists over at least about 150 residues. In an especially preferred embodiment, the percent identity exists over the entire length of the coding regions.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2: 482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48: 443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85: 2444 (1988), by  
5 computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally*, Ausubel *et al.*, *infra*).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol.*  
10 *Biol.* 215: 403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database  
15 sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching  
20 residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either  
25 sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see*  
30 Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin &

Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered  
5 similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Pre-protein: protein that is normally targeted to a cellular organelle, such as a chloroplast, and still comprises its native transit peptide.

10 Purified: the term "purified," when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the natural state. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high  
15 performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or protein is at least about 50% pure, more preferably at least about 85% pure, and most preferably at least about 99% pure.

20 Two nucleic acids are "recombined" when sequences from each of the two nucleic acids are combined in a progeny nucleic acid. Two sequences are "directly" recombined when both of the nucleic acids are substrates for recombination. Two sequences are "indirectly recombined" when the sequences are recombined using an intermediate such as a cross-over oligonucleotide. For indirect recombination, no more than one of the sequences is an actual  
25 substrate for recombination, and in some cases, neither sequence is a substrate for recombination.

"Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operatively linked to the nucleotide sequence of interest and termination signals. They also typically encompass  
30 sequences required for proper translation of the nucleotide sequence.

Significant Increase: an increase in enzymatic activity that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater



of the activity of the wild-type enzyme in the presence of the inhibitor, more preferably an increase by about 5-fold or greater, and most preferably an increase by about 10-fold or greater.

Significantly less: means that the amount of a product of an enzymatic reaction is  
5 reduced by more than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater of the activity of the wild-type enzyme in the absence of the inhibitor, more preferably an decrease by about 5-fold or greater, and most preferably an decrease by about 10-fold or greater.

Specific Binding/Immunological Cross-Reactivity: An indication that two nucleic  
10 acid sequences or proteins are substantially identical is that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, a protein is typically substantially identical to a second protein, for example, where the two proteins differ only by conservative substitutions. The phrase "specifically (or selectively) binds to an antibody," or "specifically (or selectively)  
15 immunoreactive with," when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions  
20 may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to the protein with the amino acid sequence encoded by any of the nucleic acid sequences of the invention can be selected to obtain antibodies specifically immunoreactive with that protein and not with other proteins except for polymorphic variants. A variety of immunoassay formats may be used to select antibodies specifically  
25 immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays, Western blots, or immunohistochemistry are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York "Harlow and Lane"), for a description of immunoassay formats and conditions that can be used to determine specific  
30 immunoreactivity. Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. An extensive  
5 guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes* part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at  
10 a defined ionic strength and pH. Typically, under "stringent conditions" a probe will hybridize to its target subsequence, but to no other sequences.

The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the  $T_m$  for a particular probe. An example of stringent hybridization  
15 conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (*see, Sambrook, infra,*  
20 for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, *e.g.*, more than 100 nucleotides, is 4-6x SSC at 40°C for 15 minutes. For short probes (*e.g.*, about 10 to 50 nucleotides), stringent conditions  
25 typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a  
30 specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially

identical. This occurs, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone nucleotide sequences that are homologues of reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

A "subsequence" refers to a sequence of nucleic acids or amino acids that comprise a part of a longer sequence of nucleic acids or amino acids (*e.g.*, protein) respectively.

Substrate: a substrate is the molecule that an enzyme naturally recognizes and converts to a product in the biochemical pathway in which the enzyme naturally carries out its function, or is a modified version of the molecule, which is also recognized by the enzyme and is converted by the enzyme to a product in an enzymatic reaction similar to the naturally-occurring reaction.

Transformation: a process for introducing heterologous DNA into a plant cell, plant tissue, or plant. Transformed plant cells, plant tissue, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, *e.g.*, a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

Viability: "viability" as used herein refers to a fitness parameter of a plant. Plants are assayed for their homozygous performance of plant development, indicating which proteins are essential for plant growth.

5 I. Identification of Essential *Arabidopsis thaliana* Nucleotide Sequences and Encoded Proteins Using *Ac/Ds* Transposon or T-DNA-Mediated Mutagenesis

As shown in the examples below, the essentiality of the nucleotide sequences described herein for normal plant growth and development, have been demonstrated for the first time in *Arabidopsis* using *Ac/Ds* transposon or T-DNA-mediated mutagenesis. Having  
10 established the essentiality of the function of the encoded proteins in *Arabidopsis thaliana* and having identified the nucleotide sequences encoding these essential proteins, the inventors thereby provide an important and sought after tool for new herbicide development.

*Arabidopsis* insertional mutant lines segregating for seedling lethal mutations are identified as a first step in the identification of essential proteins. Starting with T2 seeds  
15 collected from single T1 plants containing T-DNA insertions in their genomes, those lines segregating homozygous seedling lethal seedlings are identified. *Ds* transposon insertion lines are produced as described in Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), incorporated herein by reference. Starting with F3 or F4 seeds collected from single F2 or F3 kanamycin-resistant plants containing *Ds* insertions in their genomes (see Figure 3 of  
20 Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), those lines segregating homozygous seedling lethal seedlings are identified. These lines are found by placing seeds onto minimal plant growth media, which contains the fungicides benomyl and maxim, and screening for inviable seedlings after 7 and 14 days in the light at room temperature. Inviabile phenotypes include altered pigmentation or altered morphology. These phenotypes are observed either on  
25 plates directly or in soil following transplantation of seedlings.

Essential genes are also identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes or embryo. Gametophytic mutants are found by examining T1  
insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective  
30 mutants produce 25% defective seeds following self-pollination of T1 plants (see Errampalli *et al.* 1991, Plant Cell 3:149-157; Castle *et al.* 1993, Mol Gen Genet 241:504-514).

When a line is identified as segregating a seedling lethal or an embryo defective phenotype, it is determined if the resistance marker in the *Ds* transposon or T-DNA insertion co-segregates with the lethality (Errampalli *et al.* (1991) *The Plant Cell*, 3:149-157). Cosegregation analysis is done by placing the seeds on media containing the selective agent and scoring the seedlings for resistance or sensitivity to the agent. Examples of selective agents used are kanamycin, hygromycin, or phosphinothricin. About 35 resistant seedlings are transplanted to soil and their progeny are examined for the segregation of the seedling lethal. In the case in which the *Ds* transposon or T-DNA insertion disrupts an essential gene, there is co-segregation of the resistance phenotype and the seedling lethal or embryo defective phenotype in every plant. Therefore, in such a case, all resistant plants segregate a seedling lethal or embryo defective phenotype in the next generation; this result indicates that each of the resistant plants is heterozygous for the mutation and hemizygous for the T-DNA insert causing the mutation.

For the *Arabidopsis* lines showing co-segregation of the transposon-encoded or T-DNA-encoded resistance marker and the lethal phenotype, PCR-based molecular approaches such as, TAIL-PCR (Liu *et al.* (1995) *Plant J.*, 8:457-463; Liu and Whittier (1995), *Genomics*, 25:674-681), TAIL2k, vectorette PCR (Riley *et al.* (1990) *Nucleic Acids Research*, 18: 2887-2890), or the GenomeWalker™ kit (CLONTECH Laboratories, Inc., Palo Alto, CA), may be used to directly amplify the plant DNA fragments flanking the transposon or T-DNA. Each of these techniques utilizes the known sequence of the transposon or T-DNA, and can be used to recover small (less than 5 kb) fragments directly adjacent to the insertion. PCR products are isolated and their DNA sequence is determined.

Alternatively, plasmid rescue may be used to isolate the plant DNA/T-DNA border fragments. Southern blot analysis may be performed as an initial step in the characterization of the molecular nature of each insertion. Southern blots are done with genomic DNA isolated from heterozygotes and using probes capable of hybridizing with the T-DNA vector DNA. Using the results of the Southern analysis, appropriate restriction enzymes are chosen to perform plasmid rescue in order to molecularly clone *Arabidopsis thaliana* genomic DNA flanking one or both sides of the T-DNA insertion. Plasmids obtained in this manner are analyzed by restriction enzyme digestion to sort the plasmids into classes based on their digestion pattern. For each class of plasmid clone, the DNA sequence is determined.

The resulting sequences, obtained by any of the above outlined approaches, are analyzed for the presence of non-*Ds* transposon and non-T-DNA vector sequences, as appropriate. When such sequences are found, they are used to search DNA and protein databases using the BLAST and BLAST2 programs (Altschul *et al.* (1990) *J Mol. Biol.* 215: 403-410; Altschul *et al.* (1997) *Nucleic Acid Res.* 25:3389-3402, both incorporated herein by reference). Additional genomic and cDNA sequences for each gene are identified by standard molecular biology procedures.

## II. Recombinant Production Of Essential Proteins And Uses Thereof

For recombinant production of a protein of the invention in a host organism, a nucleotide sequence encoding the protein is inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of the specific regulatory sequences such as promoter, signal sequence, 5' and 3' untranslated sequence, and enhancer appropriate for the chosen host is within the level of the skill of the routineer in the art. The resultant molecule, containing the individual elements linking in the proper reading frame, is inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli*, yeast, and insect cells (see, *e.g.*, Lucknow and Summers, *Bio/Technol.* 6:47 (1988)). Additional suitable expression vectors are baculovirus expression vectors, *e.g.*, those derived from the genome of *Autographica californica* nuclear polyhedrosis virus (AcMNPV). A preferred baculovirus/insect system is PVL1392(3) used to transfect *Spodoptera frugiperda* SF9 cells (ATCC) in the presence of linear *Autographica californica* baculovirus DNA (Phramingen, San Diego, CA). The resulting virus is used to infect HighFive *Tricoplusia ni* cells (Invitrogen, La Jolla, CA).

Recombinantly produced proteins are isolated and purified using a variety of standard techniques. The actual techniques used vary depending upon the host organism used, whether the protein is designed for secretion, and other such factors. Such techniques are well known to the skilled artisan (see, *e.g.* chapter 16 of Ausubel, F. *et al.*, "Current Protocols in Molecular Biology", pub. by John Wiley & Sons, Inc. (1994).

### III. Assays For Characterizing The Essential Proteins

The recombinantly produced proteins described herein are useful for a variety of purposes. For example, they can be used in *in vitro* assays to screen known herbicidal chemicals whose target has not been identified to determine if they inhibit protein activity.

- 5 Such *in vitro* assays may also be used as more general screens to identify chemicals that inhibit such protein activity and that are therefore novel herbicide candidates. Recombinantly produced proteins may also be used to elucidate the complex structure of these molecules and to further characterize their association with known inhibitors in order to rationally design new inhibitory herbicides. Alternatively, the recombinant protein can be used to isolate  
10 antibodies or peptides that modulate the activity and are useful in transgenic solutions.

### IV. *In vitro* Inhibitor Assay: Discovery of Small Molecule Ligands That Interact with Essential Proteins Of Unknown Biochemical Function

- Once a protein has been identified as a potential herbicide target based on its  
15 essentiality for normal plant growth and viability, a next step is to develop an assay that allows screening large number of chemicals to determine which ones interact with the protein. Although it is straightforward to develop assays for proteins of known function, developing assays with proteins of unknown functions can be more difficult.

- To address this issue, novel technologies are used that can detect interactions between  
20 a protein and a compound without knowing the biological function of the protein. A short description of three methods is presented, including fluorescence correlation spectroscopy, surface-enhanced laser desorption/ionization, and biacore technologies.

- Fluorescence Correlation Spectroscopy (FCS) theory was developed in 1972 but it is only in recent years that the technology to perform FCS became available (Madge *et al.*  
25 (1972) Phys. Rev. Lett., 29: 705-708; Maiti *et al.* (1997) Proc. Natl. Acad. Sci. USA, 94: 11753-11757). FCS measures the average diffusion rate of a fluorescent molecule within a small sample volume. The sample size can be as low as  $10^3$  fluorescent molecules and the sample volume as low as the cytoplasm of a single bacterium. The diffusion rate is a function of the mass of the molecule and decreases as the mass increases. FCS can therefore be  
30 applied to protein-ligand interaction analysis by measuring the change in mass and therefore in diffusion rate of a molecule upon binding. In a typical experiment, the target to be analyzed is expressed as a recombinant protein with a sequence tag, such as a poly-histidine

sequence, inserted at the N or C-terminus. The expression takes place in *E. coli*, yeast or insect cells. The protein is purified by chromatography. For example, the poly-histidine tag can be used to bind the expressed protein to a metal chelate column such as Ni<sup>2+</sup> chelated on iminodiacetic acid agarose. The protein is then labeled with a fluorescent tag such as  
5 carboxytetramethylrhodamine or BODIPY® (Molecular Probes, Eugene, OR). The protein is then exposed in solution to the potential ligand, and its diffusion rate is determined by FCS using instrumentation available from Carl Zeiss, Inc. (Thornwood, NY). Ligand binding is determined by changes in the diffusion rate of the protein.

Surface-Enhanced Laser Desorption/Ionization (SELDI) was invented by Hutchens  
10 and Yip during the late 1980's (Hutchens and Yip (1993) Rapid Commun. Mass Spectrom. 7: 576-580). When coupled to a time-of-flight mass spectrometer (TOF), SELDI provides a mean to rapidly analyze molecules retained on a chip. It can be applied to ligand-protein interaction analysis by covalently binding the target protein on the chip and analyze by MS the small molecules that bind to this protein (Worrall *et al.* (1998) Anal. Biochem. 70: 750-  
15 756). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the SELDI chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via, for example, a delivery system capable to pipette the ligands in a sequential  
20 manner (autosampler). The chip is then submitted to washes of increasing stringency, for example a series of washes with buffer solutions containing an increasing ionic strength. After each wash, the bound material is analyzed by submitting the chip to SELDI-TOF. Ligands that specifically bind the target will be identified by the stringency of the wash needed to elute them.

25 Biacore relies on changes in the refractive index at the surface layer upon binding of a ligand to a protein immobilized on the layer. In this system, a collection of small ligands is injected sequentially in a 2-5 microlitre cell with the immobilized protein. Binding is detected by surface plasmon resonance (SPR) by recording laser light refracting from the surface. In general, the refractive index change for a given change of mass concentration at the surface  
30 layer, is practically the same for all proteins and peptides, allowing a single method to be applicable for any protein (Liedberg *et al.* (1983) Sensors Actuators 4: 299-304; Malmquist (1993) Nature, 361: 186-187). In a typical experiment, the target to be analyzed is expressed



as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the Biacore chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via the delivery system incorporated in the instruments  
5 sold by Biacore (Uppsala, Sweden) to pipette the ligands in a sequential manner (autosampler). The SPR signal on the chip is recorded and changes in the refractive index indicate an interaction between the immobilized target and the ligand. Analysis of the signal kinetics on rate and off rate allows the discrimination between non-specific and specific interaction.

10 Another assay for small molecule ligands that interact with a polypeptide is an inhibitor assay. For example, such an inhibitor assay useful for identifying inhibitors of the products of essential plant nucleic acid sequences, such as the essential *Arabidopsis* proteins described herein, comprises the steps of:

a) reacting an essential *Arabidopsis* protein described herein and a substrate thereof in  
15 the presence of a suspected inhibitor of the protein's function;

b) comparing the rate of enzymatic activity of the protein in the presence of the suspected inhibitor to the rate of enzymatic activity under the same conditions in the absence of the suspected inhibitor; and

c) determining whether the suspected inhibitor inhibits the essential *Arabidopsis*  
20 protein.

For example, the inhibitory effect on the activity of a hereindescribed essential *Arabidopsis* protein, may be determined by a reduction or complete inhibition of protein activity in the assay. Such a determination may be made by comparing, in the presence and absence of the candidate inhibitor, the amount of substrate used or intermediate or product  
25 made during the reaction.

## V. Production of peptides

Phage particles displaying diverse peptide libraries permits rapid library construction, affinity selection, amplification and selection of ligands directed against an essential protein  
30 (H.B. Lowman, *Annu. Rev. Biophys. Biomol. Struct.* 26, 401-424 (1997)). Structural analysis of these selectants can provide new information about ligand-target molecule interactions and

then in the process also provide a novel molecule that can enable the development of new herbicides based upon these peptides as leads.

#### VI. *In Vivo* Inhibitor Assay

5           In one embodiment, a suspected herbicide, for example identified by *in vitro* screening, is applied to plants at various concentrations. The suspected herbicide is preferably sprayed on the plants. After application of the suspected herbicide, its effect on the plants, for example death or suppression of growth is recorded.

10           In another embodiment, an *in vivo* screening assay for inhibitors of the activity of a hereindescribed essential protein uses transgenic plants, plant tissue, plant seeds or plant cells capable of overexpressing a nucleotide sequence disclosed herein that encodes an essential protein, wherein the essential protein is enzymatically active in the transgenic plants, plant tissue, plant seeds or plant cells. A chemical is then applied to the transgenic plants, plant tissue, plant seeds or plant cells and to the isogenic non-transgenic plants, plant tissue, plant  
15 seeds or plant cells, and the growth or viability of the transgenic and non-transformed plants, plant tissue, plant seeds or plant cells are determined after application of the chemical and compared. Compounds capable of inhibiting the growth of the non-transgenic plants, but not affecting the growth of the transgenic plants are selected as specific inhibitors of the essential protein's activity.

20           The invention will be further described by reference to the following detailed examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

#### EXAMPLES

25           Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by J. Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual, 3d Ed.*, Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (2001); by T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. *et al.*, *Current*  
30 *Protocols in Molecular Biology*, New York, John Wiley and Sons Inc., (1988), Reiter, *et al.*, *Methods in Arabidopsis Research*, World Scientific Press (1992), and Schultz *et al.*, *Plant Molecular Biology Manual*, Kluwer Academic Publishers (1998). These references describe

the standard techniques used for all steps in tagging and cloning genes from *Ac/Ds* transposon or T-DNA mutagenized populations of *Arabidopsis*: plant infection and transformation; screening for the identification of seedling mutants; and cosegregation analysis. *Ds* transposon insertion lines produced as described in Sundaresan *et al.* (1995) *Genes and Dev.*, 9:1797-1810) are used in these experiments. T-DNA lines are generated using vacuum infiltration or floral dip methods (Bechtold *et al.* (1993) *C. R. Acad. Sci. Paris*, 316:1194-1199; Clough and Bent (1998) *Plant J.*, 16:735-743; Desfeux *et al.* (2000) *Plant Physiol.*, 123:895-904).

10 Example 1: Identification of *Arabidopsis* Mutants with Lethal Phenotypes

Essential genes are identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes, embryo, or resulting seedling. Gametophytic mutants are found by examining insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective lethal mutants usually produce 25% defective seeds following self-pollination of plants heterozygous for an insertion (see Errampalli *et al.* 1991, *Plant Cell* 3:149-157; Castle *et al.* 1993, *Mol Gen Genet* 241:504-514). Seedling lethal mutants usually segregate 25% seedlings that exhibit a lethal phenotype.

20 Example 2: Cosegregation Analysis for Lines with Lethal Phenotypes

The linkage of the mutation to the *Ds* or T-DNA insertion is established after identifying a transformed line segregating for a lethal phenotype of interest. A line segregating with a single functional insert will segregate for resistance in the ratio of about 2:1 (resistant: sensitive) to the selectable marker. In the case of an embryo defective mutant, one-quarter of the progeny of a plant heterozygous for an insertion will fail to germinate due to embryo lethality, resulting in a reduction of the normal 3:1 ratio to 2:1. In the case of a seedling lethal mutant, the seedlings with a mutant phenotype are excluded in the calculation of this ratio. Each of the resistant progeny is therefore heterozygous for the mutation if the *Ds* or T-DNA insertion is causing the mutant phenotype. To establish cosegregation of the insertion and the mutant phenotype, about 30 resistant progeny are transplanted to soil and each plant is shown to segregate the 25% progeny with a lethal phenotype by the appropriate screening of embryo or seedlings. When all resistant plants segregate the lethal phenotype,

there is cosegregation of the insertion and the lethal mutation and the line is designated as "tagged."

#### Example 3: T-DNA Border Isolation by Plasmid Rescue

5        The plasmid rescue technique is used to molecularly clone *Arabidopsis* flanking DNA from one or both sides of the T-DNA insertion(s). *Arabidopsis* genomic DNA is isolated as described by Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992). Genomic DNA is digested with a restriction endonuclease and ligated overnight. After ligation, the DNA is transformed into competent *E. coli* strain XL-1 Blue, DH10B, DH5  
10    alpha, or the like, and colonies are selected on semi-solid medium containing ampicillin. Resistant colonies are picked into liquid medium with ampicillin and grown overnight. Plasmid DNA is isolated and digested with the rescue enzyme and analyzed on agarose gels containing ethidium bromide for visualization. Plasmids that represent different size classes are sequenced using primers that flank the plant DNA portion of the rescue element and the  
15    sequence is analyzed to determine what portion is plant DNA and what gene has been disrupted. The plasmid rescue is validated via PCR of template genomic DNA from a heterozygote for the insertion mutation. The experiment uses a primer anchored in the predicted flanking sequence and a primer in the T-DNA insertion. Finding a PCR product of the appropriate size, based on the sequence of the plasmid rescue clone confirms a valid  
20    rescue. Alternatively, Southern blot analysis with a probe that detects the relevant region of *Arabidopsis* DNA in genomic DNA from a heterozygote for the insertion mutation can be used to confirm the plasmid rescue results.

#### Example 4: Transposon or T-DNA Border Isolation by TAIL-PCR

25        *Arabidopsis* genomic DNA is isolated according to Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL-PCR technique (Liu *et al.* (1995) *Plant J.*, 8:457-463; Liu and Whittier (1995), *Genomics*, 25:674-681). Three sets of  
30    12 TAIL-PCR reactions, referred to as the primary, secondary and tertiary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or

T-DNA-specific primer are used. The arbitrary degenerate primer is chosen from among seven primers, LWAD1, CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers are used in combination with two sets of three, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T-DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (tertiary primer) and left borders are recovered with JM33 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (tertiary primer) and left borders are recovered with JM33 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCVICEn4HPT (Hayashi *et al.* (1992), *Science*, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) *Plant Physiol.* 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (tertiary primer). When the degenerate and nested primer pairs are used in a series of low and high-stringency PCR amplifications, as described in the TAIL-PCR protocol (Liu and Whittier (1995), *Genomics*, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon or T-DNA insertion. The nucleic acid sequences of the PCR products from the tertiary TAIL-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-*Ds* transposon or non-T-DNA vector sequence.

To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone confirms a valid rescue.

Table 1: Arbitrary Degenerate Primers

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Degen.</u>	<u>Primer Sequence</u>
101	LWAD1	1026	ngt tgw gna twt sgw gnt
102	CA50	128	ngt cga swg ana wga a
5 103	CA51	128	tgw gna gsa nca sag a
104	CA52	128	agw gna gwa nca wag g
105	CA53	256	stt gnt ast nct ntg c
106	CA54	64	ntc gas twt sgw gtt
107	CA55	256	wgt gna gwa nca nag a

10

Table 2: Nested Primers For *Ds* Lines

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Primer Sequence</u>
108	5A	actagctctaccgtttccgtttccgtttac
109	5B	ttacctcgggttcgaaatcgatcgggataa
15 110	5C	aaaatcgggttatacgataacggtcggtacggga
111	3A	gggtcttcggtatctgaatatatgtttcatgtgtg
112	3B	taccgaagaaaaafaccggtcccggtccgatttcgac
113	3C	ggatcgtatcggttttcgattaccgtatttatcc

20 Table 3: Nested Primers For T-DNA Lines

<u>SEQ ID NO:</u>	<u>Primer</u>	<u>Primer Sequence</u>
114	CA66	att agg cac ccc agg ctt tac act tta tg
115	CA67	gta tgt tgt gtg gaa ttg tga gcg gat aac
116	CA68	taa caa ttt cac aca gga aac agc tat gac
25 117	JM33	tag cat ctg aat ttc ata acc aat ctc gat aca c
118	JM34	gct tcc tat tat atc ttc cca aat tac caa tac a
119	JM35	gcc ttt tca gaa atg gat aaa tag cct tgc ttc c
120	QRB1	caa act agg ata aat tat cgc gcg cgg tgt ca
121	QRB2	ggt gtc atc tat gtt act aga tcg gga att ga
30 122	QRB3	cgc cat ggc ata tgc tag cat gca taa ttc
123	SKI1	aat tgg taa tta ctc ttt ctt ttc ctc cat att ga
124	SKI2	ata ttg acc atc ata ctc att gct gat cca t
125	SKI3	tga tcc atg tag att tcc cgg aca tga a

Example 5: Transposon or T-DNA Border Isolation by TAIL2k PCR

*Arabidopsis* genomic DNA is isolated according to Reiter *et al.* in Methods in Arabidopsis Research, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL2k PCR technique. Two sets of 12 TAIL-PCR reactions, referred to as the primary and secondary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or T-DNA-specific primer are used. The arbitrary degenerate primer is selected from among six primers; CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers are used in combination with two sets of two, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T-DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (sequencing primer) and left borders are recovered with JM33 (sequencing primer), JM34 (secondary primer), and JM35 (primary primer). Primers CA66, CA67, and CA68 are also known as RB1, RB2, and RB3, respectively. Primers JM35, JM34, and JM33 are also known as LB1, LB2, and LB3, respectively. For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (sequencing primer) and left borders are recovered with JM33 (sequencing primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCVICEn4HPT (Hayashi *et al.* (1992), Science, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) Plant Physiol. 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (sequencing primer). When the degenerate and nested primer pairs are used in a series of low and high-stringency PCR amplifications, as described in the TAIL-PCR protocol (Liu and Whittier (1995), Genomics, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon

or T-DNA insertion. TAIL2k-PCR differs from the original TAIL-PCR protocol by the elimination of the tertiary PCR and modification of the secondary PCR. The cycling conditions used in the secondary reaction are modified to include 5 high annealing temperature cycles (64 degrees C) at the beginning, three additional so-called super cycles, and five additional low annealing temperature cycles (44 degrees C) at the end of the reaction. The melting and extension times are the same as all other TAIL-PCR reactions. Additionally, the reaction volume is increased to 40 microliters. The nucleic acid sequences of the PCR products from the secondary TAIL2k-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-*Ds* transposon or non-T-DNA vector sequence.

To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL2k-PCR sequencing result confirms a valid rescue.

#### Example 6: Identification of Both Borders of a T-DNA or *Ds* Insertion

If the results of border rescue provide information on only one of the two borders for an insertion in a given line, additional experiments are performed to identify the second border. These experiments are necessary to show that a single gene has been disrupted in a given line. In some cases, an insertion can affect more than a single gene due to a chromosomal deletion or rearrangement. In those cases, additional experiments are required to identify which of the affected genes is responsible for the lethal phenotype.

When both borders of an insertion are not recovered, primers are designed to isolate a PCR product that will provide information on the location of the missing border. Three primers are chosen in *Arabidopsis* genomic DNA on the opposite side of the insertion about one, two, and five kb away from the insertion point; the primers point towards the expected second border. Long PCR conditions (Advantage 2, Clontech) are then employed following the manufacturer's directions to amplify the relevant region from genomic DNA isolated from a heterozygote for the lethal mutation. PCR reactions are performed using appropriate pairs of genomic and T-DNA or *Ds* border primers. Finding a PCR product of the appropriate size,



based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point.

If the second border is not recovered with this method, an additional set of PCR reactions are preformed. In these experiments, the genomic primers are paired with a series of internal T-DNA or *Ds* primers designed at about one kb intervals in both orientations across the entire T-DNA or *Ds* vector sequence. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point. Any borders recovered with this approach are classified as abnormal because they lack the ends of the *Ds* transposon or the expected 24 bp T-DNA imperfect repeat characteristic of right and left borders.

#### Example 7: Identification of Insertion Points for Lines with Lethal Phenotypes

For each line with a lethal phenotype, the sequences of the borders of the insertion are determined and the insertion points in the *Arabidopsis* genome are deduced. For *Ds* insertion lines, PCR products are obtained from the Ds3 and Ds5 borders. For T-DNA lines, PCR products or plasmid rescue clones are obtained from left (LB), right (RB), or abnormal (AB) borders. These sequences are used in BLASTn searches against nucleotide databases (Altschul *et al.* (1990) J Mol. Biol. 215:403-410; Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402). The results are summarized in Table 4. *Ds* line names begin with ET or GT; T-DNA line names are numbers. The insertion point (Insert Pt.) and the direction of the flanking sequence (Dir.) either up (U) or down (D) in the genome section is noted. Often, small deletions or duplications of genomic DNA accompany the insertion of a T-DNA or *Ds* transposon.

The gene that has been inactivated in a given line with a lethal phenotype is determined from the insertion points for that line. Often, the precise location of an ORF for a given gene is not known, but predictions are available in genome sections deposited in GenBank. The precise boundaries of that ORF is determined as described in Example 7.

Table 4: Insertion Points For Lines With Lethal Phenotypes

Gene	Line #	Border	Genome Section	Acc. #	Insert Pt.	Dir.
942	942	LB	K24G6	AB012242	33667	D

978	978	LB	F23N20	AC016972	58221	D
	978	LB	F23N20	AC016972	58301	U
3218	3218	LB	T8K14	AC007202	10500	D
	3218	LB	T8K14	AC007202	10540	U
4563	4563	LB	ATCHRII092	AC006438	25542	D
8794	8794	LB	F2J6	AC009526	45854	D
	8794	LB	F2J6	AC009526	45879	U
9106	9106	LB	T2J13	AL132967	78013	U
	9106	AB	T2J13	AL132967	77943	D
10708	10708	RB	F1I21	AC005687	40005	D
	10708	LB	F1I21	AC005687	40042	U
	70241	LB	F1I21	AC005687	40210	D
	70241	RB	F1I21	AC005687	40215	U
10844	10844	LB	F13F21	AC007504	60873	U
	10844	LB	F13F21	AC007504	60839	D
10951	10951	LB	MKP11	AB005238	20298	D
	10951	LB	MKP11	AB005238	20318	U
12935	12935	LB	ATCHRII150	AC005168	36510	D
	12935	LB	ATCHRII150	AC005168	36545	U
13823	11361	LB	T27G7	AC006932	78096	U
	11361	AB	T27G7	AC006932	78065	D
	13823	LB	T27G7	AC006932	78096	U
	13823	RB	T27G7	AC006932	77722	D
14519	14519	LB	ATCHRIV72	AL161576	50259	U
	14519	AB	ATCHRIV72	AL161576	50228	D
14610.1	14610.1	LB	F4P13	AC009325	55319	U
	14610.1	RB	F4P13	AC009325	55442	D
14891	14891	LB	ATCHRIV89	AL161593	11412	U
	14891	RB	ATCHRIV89	AL161593	11313	D
14986	14986	LB	K10D20	AP000410	51816	D
	14986	RB	K10D20	AP000410	54505	U
15377	15377	RB	F28G11	AC074025	19572	D
	15377	LB	F28G11	AC074025	19587	U
16219	16219	LB	MRO11	AB005244	51998	U
	16219	LB	MRO11	AB005244	51995	D
16547	16547	LB	ATCHRIV65	AL161565	80692	D
	16547	RB	ATCHRIV65	AL161565	80791	U
20933	20933	LB	ATCHRII146	AC004747	47678	D
	20933	LB	ATCHRII146	AC004747	47683	U
21455	21455	LB	ATCHRIV54	AL161554	105596	U
	21455	RB	ATCHRIV54	AL161554	105542	D
21878	21878	LB	T19F11	AC009918	19609	D
23915	23915	LB	ATCHRII008	AC005936	49629	D
	23915	LB	ATCHRII008	AC005936	49657	U
30945	30945	LB	ATCHRII192	AC004238	2411	D
	30945	LB	ATCHRII192	AC004238	2410	U

31895	31895	LB	MTI20	AB013396	52020	D
	31895	LB	MTI20	AB013396	52089	U
34269	34269	LB	T4O12	AC007396	92811	U
	34269	RB	T4O12	AC007396	92808	D
34540	34540	LB	T1G11	AC002376	41572	D
	34540	LB	T1G11	AC002376	41608	U
	72902	LB	T1G11	AC002376	41494	U
	72902	LB	T1G11	AC002376	41465	D
34555	34555	LB	T1F15	AC004393	42152	D
	54334	RB	T1F15	AC004393	41803	U
	54334	LB	T1F15	AC004393	41671	D
35154	35154	RB	MWD9	AB007651	45718	D
	35154	LB	MWD9	AB007651	45732	U
35438	35438	LB	MAL21	AP000383	25170	D
	35438	LB	MAL21	AP000383	25738	U
37351	37351	LB	F25C20	AC007296	52890	U
	37351	RB	F25C20	AC007296	52196	D
37389	37389	LB	F3F19	AC007357	45488	U
	37389	RB	F3F19	AC007357	45471	D
38108	38108	LB	ATCHRII150	AC005168	83430	D
	38108	RB	ATCHRII150	AC005168	83446	U
43301	43301	RB	T22D16	AL357612	57549	D
	43301	LB	T22D16	AL357612	57599	U
46250	46250	LB	F17A9	AC016827	74222	D
	46250	RB	F17A9	AC016827	74274	U
47050A	47050	LB	T23E18	AC009978	49445	D
	47050	RB	T23E18	AC009978	49475	U
52949A	52949	LB	K16H17	AB016884	34713	D
	52949	LB	K16H17	AB016884	34718	U
53210A	53210	RB	ATCHRII017	AC007167	92796	D
	53210	LB	ATCHRII017	AC007167	92942	U
	69121	LB	ATCHRII017	AC007167	94478	D
	69121	LB	ATCHRII017	AC007167	94502	U
55483	55483	RB	ATCHRII164	AC005727	71269	U
	55483	LB	ATCHRII164	AC005727	71258	D
58351A	58351	RB	MYH9	AB016893	42547	D
	58351	LB	MYH9	AB016893	42772	U
60944	60944	LB	F1B16	AC023754	89492	U
	60944	LB	F1B16	AC023754	89428	D
62837	62837	LB	T21J18	AL132963	70906	U
	62837	LB	T21J18	AL132963	70873	D
65310	65310	LB	T20H2	AC022472	8158	U
	65310	RB	T20H2	AC022472	8096	D
68181	68181	RB	F12A12	AL133314	38270	U
	68181	LB	F12A12	AL133314	38275	D
70913	70913	LB	T24H18	AL353013	5347	D

	70913	LB	T24H18	AL353013	5358	U
71067	71067	LB	F2E2	AC069252	63031	U
	71067	LB	F2E2	AC069252	62932	D
71654	71654	RB	MYA6	AB023046	71956	U
	71654	LB	MYA6	AB023046	71907	D
ET3172	ET3172	DS5	ATCHRIV4	AL161492	134442	U
ET3546	ET3546	DS3	ATCHRII115	AC006081	20874	D
	ET3546	DS5	ATCHRII115	AC006081	20973	U

#### Example 8: Identification of cDNAs for Essential Genes

A cDNA for a gene identified as essential is identified using a variety of approaches. This information enables the ORF for a given gene to be identified and used for other experiments including expression of the corresponding protein in heterologous systems.

If there is a full-length cDNA deposited in GenBank or published elsewhere, that sequence may be checked independently using methods described below. Alternatively, the sequence may be considered to be correct.

In some cases, there are published EST sequences that can be assembled to cover the entire ORF from start codon to stop codon. This sequence may be checked independently using methods described below or it may be considered to be correct.

Often part of the cDNA is published and this information can be used to identify the entire ORF. If the 5' end containing the start codon is known, 3' RACE is performed to identify the remainder of the cDNA. If the 3' end containing the stop codon is known, 5' RACE is performed to identify the remainder of the cDNA. If both the 5' and the 3' ends are known, but the sequence between the two ends of the cDNA is not known, PCR is performed with primers hybridizing to each end of the cDNA. In all three of these cases, PCR is performed using template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

If no part of the cDNA is published, the cDNA is identified by starting from gene model predictions in the annotation for genomic clones or elsewhere. To identify the ORF, primers are designed to the 5' and 3' ends of the predicted ORF. PCR is performed using template DNA from a cDNA library prepared from seedling tissue or the pFL61 *Arabidopsis* cDNA library (Minet *et al.* (1992) Plant J. 2: 417-422). The resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced. Alternatively, 5' and 3' RACE are performed with primers predicted by gene models to be in exons. PCR is performed using

template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

- If the cDNA sequence is the same as the sequence predicted in the GenBank annotation, the experiments confirm for the first time the actual ORF. If the cDNA sequence is not the same as the sequence predicted in the GenBank annotation, the experiments identify for the first time the actual ORF. In some cases, more than one cDNA sequence is found for a given gene and both sequences are included in this application.

#### 10 Example 9: Description of Essential Genes

- The putative function of the protein encoded by each essential gene is determined from analysis of the ORF in each cDNA. Information from the relevant *Arabidopsis* genomic section deposited in GenBank is used as a starting point to explore the function of a given gene. This analysis also includes BLAST searches (Altschul *et al.* (1990) J. Mol. Biol. 215:403-410; Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402) of sequence databases to identify similar proteins. Table 5 describes the putative functions for the essential genes discovered in this application.

Table 5: Putative Functions For Essential Genes

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Gene	SEQ ID Nos:	Putative Function & Similar Genes	References
00942	1-2	similarity to disease resistance protein large gene family in <i>Arabidopsis</i> including disease resistance proteins RPP1-WsA,B&C; similar to tobacco TMV resistance protein N	Whitham, S. <i>et al.</i> (1994) Cell 78:1101-1115; Botella, M.A., <i>et al.</i> (1998) Plant Cell 10: 1847-1860
00978	3-4	unknown protein similar to <i>Arabidopsis</i> protein of unknown function (CAB87660) & ESTs from many plants	none
03218	5-6	AAA ATPase similar to <i>E. coli</i> FtsH cell division protein (P28691) that acts as an ATP-dependent metalloproteinase; homologs in many species	Schumann, W. (1999) FEMS Microbiol Rev 23:1-11; Langer, T. (2000) Trends Biochem Sci 25:247-251

04563	7-8	unknown protein large gene family in <i>Arabidopsis</i> of unknown function proteins	none
08794	9-10	putative histidine decarboxylase similar to Brassica, tomato (tom92), and rice putative histidine decarboxylases	Picton, S <i>et al.</i> (1993) <i>Plant Mol Biol</i> 23:627-631; Watanabe, T <i>et al.</i> (1990) <i>Trends Pharmacol Sci</i> 11:363- 367; Vaaler, G.L. & Snell, E.E. (1989) <i>Biochemistry</i> 28:7306-7313
09106	11-12	cytosolic 40S ribosomal protein S11-alpha	Browning, K.S. (1996) <i>Plant Mol Biol</i> 32:107-144; Gantt, J. S. & Thompson, M.D. (1990) <i>J. Biol Chem</i> 265:2763-2767
10708	13-14	cytoplasmic 60S ribosomal protein L3	Peltz, S.W. <i>et al.</i> (1999) <i>Mol Cell Biol</i> 19:384-391; Kim, Y. <i>et al.</i> (1990) <i>Gene</i> 93:177- 182; Wickner, R.B <i>et al.</i> (1982) <i>Proc Natl Acad Sci USA</i> 79:4706-4708
10844	15-16	40S ribosomal protein S17-like	Gantt, J.S. & Thompson, M.D. (1990) <i>J Biol Chem</i> 265:2763- 2767; Wiener, L. <i>et al.</i> (1988) <i>Nucleic Acids Res</i> 16:1233- 1250
10951	17-18	phytoene synthase	Welsch, R. <i>et al.</i> (2000) <i>Planta</i> 211:846-854; Shewmaker, C.K. <i>et al.</i> (1999) <i>Plant J.</i> 20:401-412; Von Lintig, J. <i>et al.</i> (1997) <i>Plant J.</i> 12:625-634
12935	19-20	putative choline kinase similar to soybean choline kinase (T08815) and mouse & human choline/ethanolamine kinases	Monks, D.E. <i>et al.</i> (1996) <i>Plant Physiol.</i> 110:1197-1205; Bligny, R. <i>et al.</i> (1989) <i>J Biol Chem.</i> 264:4888-4895; Wharfe, J. & Harwood, J.L. (1979) <i>Biochim Biophys Acta.</i> 575:102-111
13823	21-22	magnesium protoporphyrin IX chelatase subunit D	Papenbrock, J. <i>et al.</i> (1997) <i>Plant J.</i> 12:981-990; Papenbrock, J. <i>et al.</i> (2000) <i>Plant Physiol.</i> 122:1161-1169; Luo, M. <i>et al.</i> (1999) <i>Plant Mol Biol.</i> 41:721-731; Jensen, P.E. <i>et al.</i> (1996) <i>Mol. Gen.</i> <i>Genet.</i> 250:383-394

14519	23-24	putative protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
14610.1	25-26	putative cell division control protein; similar to cdc48, AAA ATPase proteins similar to <i>S. pombe</i> AAA ATPase (CAB16902); <i>Arabidopsis</i> cdc48 homolog (P54609); cdc48/valosin- containing protein homologs from soybean, <i>Capsicum annuum</i> , rice, <i>Dictyostelium</i> ; <i>Drosophila</i> smallminded	Frohlich, K.U. <i>et al.</i> (1991) J Cell Biol. 114:443-453; Feiler, H.S. <i>et al.</i> (1995) EMBO J. 14:5626-5637; Langer, T. (2000) Trends Biochem Sci 2000 25:247-251
14891	27-28	putative protein contains PFAM 02536 mTERF (mitochondrial transcription termination factor) domain; large gene family in <i>Arabidopsis</i> of unknown function proteins	Fernandez-Silva, P. <i>et al.</i> (1997) EMBO J 16:1066-1079
14986	29-30	ubiquitin isopeptidase T (aka ubiquitin-specific protease 14)	Wilkinson, K.D. <i>et al.</i> (1995) Biochemistry 34:14535- 14546; Falquet, L. <i>et al.</i> (1995) FEBS Lett 376:233- 237; Lindsey, D.F. <i>et al.</i> (1998) J Biol Chem 273:29178-29187
15377	31-32	putative formyl transferase similar to <i>B. napus</i> methionyl tRNA transformylase Fmt protein (AJ245479) & <i>B. rapa</i> S-locus protein 8 (AB022076)	Cui Y <i>et al.</i> (1999) Plant Cell. 11:2217-2231; Suzuki, G. <i>et al.</i> (1999) Genetics 153:391- 400; Cusack S. (1999) Curr Opin Struct Biol. 9:66-73
16219	33-34	polyadenylation cleavage/specificity factor 100 kDa subunit (AF283277)	Bilger, A. <i>et al.</i> (1994) Genes Dev. 8:1106-1116; Bienroth, S. <i>et al.</i> (1993) EMBO J. 12:585-594; Jenny, A. <i>et al.</i> (1994) Mol Cell Biol. 14:8183-8190
16547	35-36	similarity to UV-induced protein Uvi31, <i>S. pombe</i> , G1381578 unknown function, but similar to <i>Pectobacterium chrysanthemi</i> SufE protein (AJ301654) involved in iron metabolism, <i>S. pombe</i> uvi31 protein of the BolA / YRBA family (Q12238), <i>Synechocystis</i> hypothetical 17.7 KDA protein SLR1419 (P74523)	Kim, S.H. <i>et al.</i> (1997) Environ Mol Mutagen 30:72- 81; Santos, J.M. <i>et al.</i> (1999) Mol Microbiol 32:789-798

20933	37-38	hypothetical protein contains WD40 repeats, similar to human CIAO 1 gene (O76071) & <i>S. cerevisiae</i> YDR267c (S70127)	Neer, E.J. <i>et al.</i> (1994) <i>Nature</i> 371:297-300; Johnstone, R.W. <i>et al.</i> (1998) <i>J Biol Chem</i> 273:10880-10887
21455	39-40	putative protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
21878	41-42	<i>Arabidopsis</i> digalactosyldiacylglycerol synthase (DGD1, AAD42378)	Dormann, P. <i>et al.</i> (1999) <i>Science</i> 284:2181-2184; Hartel, H. <i>et al.</i> (1997) <i>Plant</i> <i>Physiol</i> 115:1175-1184
23915	43-44	hypothetical protein contains PPR motifs, member of large gene family in <i>Arabidopsis</i>	Small, I.D. & Peeters, N. (2000) <i>Trends Biochem Sci</i> 25:46-47; Manthey, G.M. & McEwen, J.E. (1995) <i>EMBO J</i> 14:4031-4043; Barkan, A. <i>et</i> <i>al.</i> (1994) <i>EMBO J</i> 13:3170- 3181
30945	45-46	unknown protein similar to rice hypothetical protein (BAB56056)	none
31895	47-48	similar to unknown protein small gene family in <i>Arabidopsis</i> of unknown function proteins	none
34269	49-50	unknown protein	none
34540	51-52	probable lipoate protein ligase B, similar to Mycobacterium LIPB gene (O32961) also similar to <i>S. pombe</i> putative pre-tRNA/pre-rRNA processing protein (T41635)	Reed, K.E. & Cronan, J.E. Jr. (1993) <i>J Bacteriol</i> 175:1325- 1336; Chen, X.J. (1997) <i>Mol.</i> <i>Gen. Genet.</i> 255:341-349
34555	53-54	similar to Synechocystis hypothetical 41.9KD protein (P52640) similar to several prokaryotic proteins of unknown function including <i>E. coli</i> YJEQ (P39286)	none
35154	55-56	similar to unknown protein similar to human hypothetical protein (BAA91556), <i>S. cerevisiae</i> probable membrane protein YOR262w (S67159), & <i>S. pombe</i> ATP(GTP)-binding protein Fet5 (AAC49837)	Shpakovskii, G.V. & Lebedenko, E.N. (1997) <i>Bioorg. Khim.</i> 23:234-237
35438	57-58	unknown protein weak similarity to <i>Pennisetum</i> <i>ciliare</i> unknown function protein (AAK15504)	none



37351	59-60	strong similarity to obtusifolios 14-alpha demethylase (CYP51; P93846) from <i>Sorghum bicolor</i> (also wheat & rice), member of the PFI00067 cytochrome P450 family	Kushiro, M. <i>et al.</i> (2001) Biochem Biophys Res Commun. 285:98-104; Bak <i>et al.</i> (1997) Plant J. 11:191-201; Grausem, B. (1995) Plant J. 7:761-770
37389	61-62	similar to human GLE1-like required for poly(A)+ RNA export (AAC25561)	Watkins, J.L. <i>et al.</i> (1998) Proc. Natl. Acad. Sci. U.S.A. 95:6779-6784; Murphy, R. & Went, S.R. (1996) Nature 383:357-360
38108	63-64	<i>Arabidopsis</i> 4-(cytidine 5'-phospho)-2-C-methyl-D-erythritol kinase (aka ispE & 4-diphosphocytidyl-2-C-methyl-Derythritol kinase) (AF288615) similar to <i>E. coli</i> ychB (aka ispE) gene (P24209)	Rohdich, F. <i>et al.</i> (2000) Proc Natl Acad Sci U.S.A. 97:8251-8256; Luetgen, H. <i>et al.</i> (2000) Proc. Natl. Acad. Sci. U.S.A. 97:1062-1067; Lange, B.M. & Croteau, R. (1999) Proc Natl Acad Sci U.S.A. 96:13714-13719
43301	65-66	similar to hypothetical bacterial proteins, including <i>Pseudomonas aeruginosa</i> protein PA0292 (F83608) & <i>Lactococcus lactis</i> (AAK05795)	none
46250	67-68	hypothetical protein weak similarity to hypothetical proteins from <i>Arabidopsis</i> (AAG51506) and mouse (BAB23375)	none
47050A	69-70	unknown protein weak similarity to Botrytis cDNA (AL115827)	none
52949A	71-72	6-phosphogluconolactonase-like protein similar to 6-phosphogluconolactonases such as human (O95336), <i>Brassica carinata</i> (AAK50346), & <i>Mycobacterium tuberculosis</i> (devB, CAB09261)	Collard, F. <i>et al.</i> (1999) FEBS Lett. 459:223-226; Bauer, H.P. <i>et al.</i> (1983) Eur J Biochem. 133:163-168
53210A	73-74	putative heat shock protein in hsp90 family similar to rye hsp82 (S65776), <i>Ipomoea nil</i> hsp83 (P51819), chicken hsp90 beta (Q04619) and others	Felsheim, R.F. & Das, A. (1992) Plant Physiol. 100:1764-1771; Coates, A.R. <i>et al.</i> (1999) Biotechnol Genet Eng Rev 16:393-405; Milioni, D. & Hatzopoulos, P. (1997) Plant Mol Biol 35:955-961

55483	75-76	putative para-aminobenzoate synthase and glutamine amidotransferase, a bifunctional enzyme similar to <i>Streptomyces pristinaespiralis</i> papA (AAC44866), <i>E. coli</i> pabB (P05041) & pabA (P00903), and <i>Bacillus stearothermophilus</i> anthranilate synthase component I trpE (AAD33791)	Goncharoff, P. & Nichols, B.P. (1984) <i>J Bacteriol.</i> 159:57-62.; Roux, B. & Walsh, C.T. (1992) <i>Biochemistry.</i> 31:6904-6910; Kaplan, J.B. & Nichols, B.P. (1983) <i>J Mol Biol</i> 168:451-468
58351A	77-78	26S proteasome p55 protein-like similar to human 26S proteasome regulatory complex chain p55 (BAA19749), <i>S. cerevisiae</i> 26S proteasome regulatory complex chain RPN5 (S67695), and others	Saito, A. <i>et al.</i> (1997) <i>Gene</i> 203:241-250; Glickman, M.H. <i>et al.</i> (1998) <i>Mol Cell Biol</i> 18:3149-3162
60944	79-80	similar to <i>Guillardia theta</i> chloroplast 50S ribosomal protein L31 (O46917)	Yamaguchi, K. & Subramanian, A.R. (2000) <i>J Biol Chem</i> , 275:28466-28482
62837	81-82	AtClpC: regulatory subunit of Clp protease with ATPase activity (BAA82062)	Adam, Z. (2000) <i>Biochimie</i> 82:647-654; Sokolenko, A. <i>et al.</i> (1998) <i>Planta</i> 207:286-295; Nakabayashi, K. <i>et al.</i> (1999) <i>Plant Cell Physiol.</i> 40:504-514; Maurizi, M.R. <i>et al.</i> (1990) <i>J Biol Chem.</i> 265:12536-12545
65310	83-84	26S proteasome regulatory subunit S3, contains a PCI PF101399 domain similar to 26S proteasome regulatory subunit S3 from <i>Nicotiana tabacum</i> (P93768), carrot (Q06364), human (O43242), <i>S. cerevisiae</i> RPN3 (P40016), and others	Voges, D. <i>et al.</i> (1999) <i>Ann Rev Biochem</i> 68:1015-1068; Fu, H. <i>et al.</i> (1999) <i>Mol Biol Rep</i> 26:137-146; Fu, H. <i>et al.</i> (1999) <i>Plant J</i> 18:529-539; Kominami, K. <i>et al.</i> (1997) <i>Mol Biol Cell</i> 8:171-187
68181	85-86	small zinc finger-like protein TIM9 similar to mitochondrial import inner membrane translocase subunit TIM9 from several plants and <i>S. cerevisiae</i> (O74700)	Koehler, C.M. <i>et al.</i> (1998) <i>EMBO J.</i> 17:6477-6486; Tokatlidis, K. <i>et al.</i> (2000) <i>Biochem Soc Trans</i> 28:495-499
70913	87-88	<i>Arabidopsis</i> CCAAT binding protein/transcription factor Hap2a (CAA74048)	Edwards, D. <i>et al.</i> (1998) <i>Plant Physiol</i> 117:1015-1022; Albani, D. & Robert, L.S. (1995) <i>Gene</i> 167:209-213

71067	89-90	hypothetical protein gene family in <i>Arabidopsis</i> of unknown function proteins	none
71654	91-92	poly(A) binding protein-like	Hilson, P. <i>et al.</i> (1993) <i>Plant Physiol</i> 103:525-533; Belostotsky, D.A. & Meagher, R.B. (1993) <i>Proc Natl Acad Sci U.S.A.</i> 90:6686-6690; Gallie, D.R. (1998) <i>Gene</i> 216:1-11
ET3172	93-94	hypothetical protein small gene family in <i>Arabidopsis</i> (T47999 & T02193) of unknown function	none
ET3546	95-96	cdc27/nuc2-like protein, may contain TPR-repeat similar to human cdc27 (P30260), <i>S. pombe</i> nuc2 (P10505), <i>S. cerevisiae</i> cdc23 (P16522), and others	Hirano, T. <i>et al.</i> (1988) <i>J. Cell Biol.</i> 106:1171-1183; Chen, P.L. <i>et al.</i> (1995) <i>Cell Growth Differ.</i> 6:199-210

#### Example 10: Expression of Recombinant Essential Proteins in *E. coli*

The coding region of each of the essential proteins, corresponding to cDNA clones of odd-numbered SEQ ID NO:1-96, is subcloned into an appropriate expression vector, and transformed into *E. coli* using the manufacturer's conditions. Specific examples include plasmids such as pBluescript (Stratagene, La Jolla, CA), pFLAG (International Biotechnologies, Inc., New Haven, CT), and pTrcHis (Invitrogen, La Jolla, CA). *E. coli* is cultured, and expression of the essential protein is confirmed. Recombinant protein is isolated using standard techniques.

#### Example 11: *In Vitro* Binding Assays

Recombinant protein for each of the essential genes described in this application is obtained, for example, according to Example 10. The protein is immobilized on chips appropriate for ligand binding assays using techniques that are well known in the art. The protein immobilized on the chip is exposed to sample compound in solution according to methods well known in the art. While the sample compound is in contact with the immobilized protein, measurements capable of detecting protein-ligand interactions are conducted. Examples of such measurements are SELDI, biacore and FCS, described above. Compounds

found to bind the protein are readily discovered in this fashion and are subjected to further characterization.

The above-disclosed embodiments are illustrative. This disclosure of the invention  
5 will place one skilled in the art in possession of many variations of the invention. All such  
obvious and foreseeable variations are intended to be encompassed by the present invention.

CLAIMS:

1. A method of identifying a herbicidal compound, comprising:
  - a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind to said polypeptide, under conditions conducive to binding;
  - b) selecting a compound identified in (a) that binds to said polypeptide;
  - c) applying a compound selected in (b) to a plant to test for herbicidal activity; and
  - d) selecting a compound identified in (c) that has herbicidal activity.
2. The method according to claim 1, wherein said polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
3. The method according to claim 2, wherein said polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
4. The method according to claim 3, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
5. A method of identifying a herbicidal compound, comprising:
  - c) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit the activity of said polypeptide, under conditions conducive to inhibition;
  - d) selecting a compound identified in (a) that inhibits the activity of said polypeptide;
  - c) applying a compound selected in (b) to a plant to test for herbicidal activity; and
  - d) selecting a compound identified in (c) that has herbicidal activity.

6. The method according to claim 5, wherein said polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
- 5 7. The method according to claim 6, wherein said polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
8. The method according to claim 7, wherein said polypeptide comprises an amino acid  
10 sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.
9. A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 1.
- 15 10. A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 5.

## SEQUENCE LISTING

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<120> NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

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<151> 2001-07-16

<150> US 60/358,416

<151> 2002-02-20

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att ccg ttg atg gct att tta ttg cct cca atg tat aca cat tcc act 576  
 Ile Pro Leu Met Ala Ile Leu Leu Pro Pro Met Tyr Thr His Ser Thr  
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tat tgg cta tgg gct gca ggg ttc tat ctc tta gcc aag gtg gaa gaa 624  
 Tyr Trp Leu Trp Ala Ala Gly Phe Tyr Leu Leu Ala Lys Val Glu Glu  
 195 200 205

gct gcg gat aag cct ata tat agc tgg act cat cat att att agt ggg 672  
 Ala Ala Asp Lys Pro Ile Tyr Ser Trp Thr His His Ile Ile Ser Gly  
 210 215 220

cat tct ctg aag cat ttg tgt gcc gct atg gtc cct gtc ttc ctt acc 720  
 His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr  
 225 230 235 240

ctc atg ctt gcg aaa aga acc gtt caa act gag agg att agc ttg tat 768  
 Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr  
                   245                                  250                                  255

aag aca tgg aag aaa gga tcc gag gaa gaa cgg ttc gag cat agc tac 816  
 Lys Thr Trp Lys Lys Gly Ser Glu Glu Glu Arg Phe Glu His Ser Tyr  
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                   20                                  25                                  30

His Asn Phe Ala Asp Gln Arg Ser Phe Phe Gly Ile Pro Asn Phe Leu  
                   35                                  40                                  45

Asn Val Ile Ser Asn Phe Pro Phe Leu Ile Ile Gly Phe Ile Gly Leu  
                   50                                  55                                  60

Ile Leu Cys Phe Tyr Pro Glu Asp Tyr Phe Ser Phe Ser Leu Arg Gly  
 65                                  70                                  75                                  80

Glu Lys Ile Gly Trp Thr Cys Phe Tyr Ile Gly Val Ala Ala Val Ala  
                   85                                  90                                  95

Phe Gly Ser Ser Tyr Tyr His Leu His Pro Asn Asp Ala Thr Leu Leu  
                   100                                  105                                  110

Trp Asp Arg Leu Pro Met Thr Ile Ala Phe Thr Ser Ile Met Ala Ile  
                   115                                  120                                  125

Phe Val Ile Glu Arg Ile Asp Glu His Lys Gly Thr Tyr Ser Ile Ala  
                   130                                  135                                  140

Pro Leu Leu Leu Ala Gly Leu Val Ser Ile Leu Tyr Trp Arg Phe Phe  
 145 150 155 160

Asp Asp Leu Arg Pro Tyr Ala Leu Val Gln Phe Val Pro Cys Ile Val  
 165 170 175

Ile Pro Leu Met Ala Ile Leu Leu Pro Pro Met Tyr Thr His Ser Thr  
 180 185 190

Tyr Trp Leu Trp Ala Ala Gly Phe Tyr Leu Leu Ala Lys Val Glu Glu  
 195 200 205

Ala Ala Asp Lys Pro Ile Tyr Ser Trp Thr His His Ile Ile Ser Gly  
 210 215 220

His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr  
 225 230 235 240

Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr  
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Lys Thr Trp Lys Lys Gly Ser Glu Glu Glu Arg Phe Glu His Ser Tyr  
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act	cag	ttg	ttg	aaa	aga	tca	aaa	agt	ttt	ggt	ctt	gtt	cgg	ttt	ccc		96
Thr	Gln	Leu	Leu	Lys	Arg	Ser	Lys	Ser	Phe	Gly	Leu	Val	Arg	Phe	Pro		
			20					25					30				
gcc	aag	tat	gga	ctg	gga	gct	acc	cgg	aaa	aaa	cag	ctc	ttt	cga	gtc		144
Ala	Lys	Tyr	Gly	Leu	Gly	Ala	Thr	Arg	Lys	Lys	Gln	Leu	Phe	Arg	Val		
			35				40					45					
tat	gcg	tct	gaa	agt	agt	agt	ggg	tct	tca	tct	aat	agc	gat	gga	ggc		192
Tyr	Ala	Ser	Glu	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Asn	Ser	Asp	Gly	Gly		
	50					55					60						
ttt	tcg	tgg	gtg	aga	ttg	gct	cag	tct	att	cgc	ctt	ggt	gcc	gag	cgg		240
Phe	Ser	Trp	Val	Arg	Leu	Ala	Gln	Ser	Ile	Arg	Leu	Gly	Ala	Glu	Arg		
65					70					75				80			
att	ggg	gag	aag	att	gga	gaa	tct	gtg	aag	aca	gaa	att	ggg	ttt	gac		288
Ile	Gly	Glu	Lys	Ile	Gly	Glu	Ser	Val	Lys	Thr	Glu	Ile	Gly	Phe	Asp		
				85					90					95			
tcg	gaa	gaa	gca	agt	ggg	aga	gtg	aat	gag	tat	gtg	gct	cga	ggt	aag		336
Ser	Glu	Glu	Ala	Ser	Gly	Arg	Val	Asn	Glu	Tyr	Val	Ala	Arg	Val	Lys		
			100					105					110				
gat	agt	gtg	cac	aag	ggc	cat	cac	gag	ctg	act	cgc	ttt	aag	aat	gag		384
Asp	Ser	Val	His	Lys	Gly	His	His	Glu	Leu	Thr	Arg	Phe	Lys	Asn	Glu		
		115					120					125					
aca	gtg	cct	tcg	ttt	att	gat	tgg	aac	aag	tgg	gag	cat	tgg	aag	gac		432
Thr	Val	Pro	Ser	Phe	Ile	Asp	Trp	Asn	Lys	Trp	Glu	His	Trp	Lys	Asp		
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atc	agg	aat	tgg	gac	ggg	aaa	cga	gtt	gct	gcc	ttg	ttc	ata	tat	gct		480
Ile	Arg	Asn	Trp	Asp	Gly	Lys	Arg	Val	Ala	Ala	Leu	Phe	Ile	Tyr	Ala		
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ttt	gcg	ctg	tta	ctt	tct	tgt	caa	aga	gtt	tat	gtt	gcc	atc	caa	gct		528
Phe	Ala	Leu	Leu	Leu	Ser	Cys	Gln	Arg	Val	Tyr	Val	Ala	Ile	Gln	Ala		
				165					170					175			
cct	cgg	gta	gaa	cga	gag	aga	aga	gag	tta	aca	gag	tct	ttt	atg	gag		576
Pro	Arg	Val	Glu	Arg	Glu	Arg	Arg	Glu	Leu	Thr	Glu	Ser	Phe	Met	Glu		
			180					185					190				
gct	ttg	atc	ccc	gag	cca	tct	cct	gga	aat	ata	gaa	aag	ttc	aag	aga		624
Ala	Leu	Ile	Pro	Glu	Pro	Ser	Pro	Gly	Asn	Ile	Glu	Lys	Phe	Lys	Arg		
			195				200					205					
aat	atg	tgg	agg	aaa	gca	aca	cct	aaa	ggc	ttg	aaa	tta	aaa	agg	ttc		672
Asn	Met	Trp	Arg	Lys	Ala	Thr	Pro	Lys	Gly	Leu	Lys	Leu	Lys	Arg	Phe		
		210				215					220						
att	gaa	gcg	cct	gat	gga	aca	ctt	gtc	cac	gat	agt	tct	tat	gtt	gga		720
Ile	Glu	Ala	Pro	Asp	Gly	Thr	Leu	Val	His	Asp	Ser	Ser	Tyr	Val	Gly		
225						230				235					240		
gaa	aat	gcg	tgg	gat	gac	gat	cta	gag	acc	aca	gag	gga	tct	ctc	aag		768

Glu Asn Ala Trp Asp Asp Asp Leu Glu Thr Thr Glu Gly Ser Leu Lys	
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aaa ata att ggt aga aat gct agg att cag aca gag gca aag aag aaa	816
Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys	
260	265 270
cta agc caa gat ctg ggt gtc tct ggt gaa att gga gac agt gta ggt	864
Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly	
275	280 285
aat tgg cgg gaa agg ctt gca acc tgg aag gaa atg tta gaa cga gaa	912
Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu	
290	295 300
aaa tta tca gaa cag tta aac tcc tca gcg gcg aag tat gtg gtt gaa	960
Lys Leu Ser Glu Gln Leu Asn Ser Ser Ala Ala Lys Tyr Val Val Glu	
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ttt gat atg aaa gag gta gag aaa agt ctt cgc gaa gat gtt att gga	1008
Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly	
325	330 335
agg aca tct gaa act gag gga act aga gct ctc tgg ata tca aag aga	1056
Arg Thr Ser Glu Thr Glu Gly Thr Arg Ala Leu Trp Ile Ser Lys Arg	
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tgg tgg cga tat cgc cct aag ctt ccc tat acc tac ttc ctt cag aag	1104
Trp Trp Arg Tyr Arg Pro Lys Leu Pro Tyr Thr Tyr Phe Leu Gln Lys	
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ctt gat tct tct gag gtt gca gct gtt gtt ttc acg gaa gac cta aag	1152
Leu Asp Ser Ser Glu Val Ala Ala Val Val Phe Thr Glu Asp Leu Lys	
370	375 380
aga ttg tat gtg acc atg aaa gaa ggt ttc cct cta gaa tat att gtt	1200
Arg Leu Tyr Val Thr Met Lys Glu Gly Phe Pro Leu Glu Tyr Ile Val	
385	390 395 400
gac att ccc tta gat cct tac ttg ttt gag act att tgc aac gcc gga	1248
Asp Ile Pro Leu Asp Pro Tyr Leu Phe Glu Thr Ile Cys Asn Ala Gly	
405	410 415
gtt gag gtg gat ctt ctt cag aag agg cag atc cac tac ttc atg aaa	1296
Val Glu Val Asp Leu Leu Gln Lys Arg Gln Ile His Tyr Phe Met Lys	
420	425 430
gtt ttc att gca ctt ctg ccg ggg ata cta att tta tgg ttt ata aga	1344
Val Phe Ile Ala Leu Leu Pro Gly Ile Leu Ile Leu Trp Phe Ile Arg	
435	440 445
gaa tct gcc atg ctt ctc ctt atc aca tcc aag cgc ttt ctc tac aag	1392
Glu Ser Ala Met Leu Leu Leu Ile Thr Ser Lys Arg Phe Leu Tyr Lys	
450	455 460
aag tat aat cag ctg ttt gat atg gct tat gca gaa aat ttt ata ttg	1440
Lys Tyr Asn Gln Leu Phe Asp Met Ala Tyr Ala Glu Asn Phe Ile Leu	
465	470 475 480
ccg gtt gga gat gtc agt gag aca aaa tca atg tat aag gaa gtg gta	1488

Pro Val Gly Asp Val Ser Glu Thr Lys Ser Met Tyr Lys Glu Val Val	
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cta ggc ggt gat gtc tgg gat ctt ctt gat gag cta atg atc tac atg	1536
Leu Gly Gly Asp Val Trp Asp Leu Leu Asp Glu Leu Met Ile Tyr Met	
500 505 510	
ggg aac cca atg caa tac tat gaa aaa gat gtg gct ttt gtc agg ggt	1584
Gly Asn Pro Met Gln Tyr Tyr Glu Lys Asp Val Ala Phe Val Arg Gly	
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gtg ctt ctt tct gga cct cct gga act gga aaa aca ctt ttt gcg cga	1632
Val Leu Leu Ser Gly Pro Pro Gly Thr Gly Lys Thr Leu Phe Ala Arg	
530 535 540	
aca ctt gca aag gaa agt ggg cta cca ttt gtg ttt gca tct ggt gcg	1680
Thr Leu Ala Lys Glu Ser Gly Leu Pro Phe Val Phe Ala Ser Gly Ala	
545 550 555 560	
gag ttc aca gac agt gaa aaa agt ggt gct gca aag atc aat gag atg	1728
Glu Phe Thr Asp Ser Glu Lys Ser Gly Ala Ala Lys Ile Asn Glu Met	
565 570 575	
ttt tca atc gcg aga cga aat gcc cct gct ttt gtg ttt gtg gat gaa	1776
Phe Ser Ile Ala Arg Arg Asn Ala Pro Ala Phe Val Phe Val Asp Glu	
580 585 590	
ata gat gct att gct ggt aga cat gct aga aaa gat cca cgg aga aga	1824
Ile Asp Ala Ile Ala Gly Arg His Ala Arg Lys Asp Pro Arg Arg Arg	
595 600 605	
gca act ttt gaa gct tta att gcg caa ctc gat ggg gag aaa gag aag	1872
Ala Thr Phe Glu Ala Leu Ile Ala Gln Leu Asp Gly Glu Lys Glu Lys	
610 615 620	
aca ggt atc gat agg ttt tct ttg aga caa gct gtg ata ttt atc tgt	1920
Thr Gly Ile Asp Arg Phe Ser Leu Arg Gln Ala Val Ile Phe Ile Cys	
625 630 635 640	
gct acc aat aga cct gat gaa ctc gac ctt gag ttt gtc cgt tct ggc	1968
Ala Thr Asn Arg Pro Asp Glu Leu Asp Leu Glu Phe Val Arg Ser Gly	
645 650 655	
cgt att gac cgt cgg ctg tat att ggg ttg cct gat gca aag caa agg	2016
Arg Ile Asp Arg Arg Leu Tyr Ile Gly Leu Pro Asp Ala Lys Gln Arg	
660 665 670	
gtg caa ata ttt gga gtt cac agt gct ggg aag aac ctt gca gaa gat	2064
Val Gln Ile Phe Gly Val His Ser Ala Gly Lys Asn Leu Ala Glu Asp	
675 680 685	
ata gac ttt ggg aag ctt gtt ttt cga acg gtt ggc ttt tcc ggg gca	2112
Ile Asp Phe Gly Lys Leu Val Phe Arg Thr Val Gly Phe Ser Gly Ala	
690 695 700	
gat atc cgg aat ctt gtt aac gaa gcg gct ata atg tcg gta agg aag	2160
Asp Ile Arg Asn Leu Val Asn Glu Ala Ala Ile Met Ser Val Arg Lys	
705 710 715 720	
gga cgt tct tac ata tat caa caa gac att gtt gat gtg tta gat aaa	2208

Gly	Arg	Ser	Tyr	Ile	Tyr	Gln	Gln	Asp	Ile	Val	Asp	Val	Leu	Asp	Lys		
				725					730					735			
caa	ttg	ctc	gag	ggg	atg	ggg	gta	ctt	ctt	aca	gag	gaa	gag	caa	cag		2256
Gln	Leu	Leu	Glu	Gly	Met	Gly	Val	Leu	Leu	Thr	Glu	Glu	Glu	Gln	Gln		
			740					745					750				
aaa	tgt	gaa	caa	agt	gta	tct	tac	gaa	aag	aag	aga	ctt	ctg	gct	gtt		2304
Lys	Cys	Glu	Gln	Ser	Val	Ser	Tyr	Glu	Lys	Lys	Arg	Leu	Leu	Ala	Val		
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cat	gag	gct	ggg	cat	ata	gtg	ttg	gct	cat	ttg	ttt	cct	cga	ttt	gac		2352
His	Glu	Ala	Gly	His	Ile	Val	Leu	Ala	His	Leu	Phe	Pro	Arg	Phe	Asp		
	770					775					780						
tgg	cat	gca	ttt	tcg	cag	ctc	ctt	cct	ggg	ggc	aag	gaa	act	gct	gta		2400
Trp	His	Ala	Phe	Ser	Gln	Leu	Leu	Pro	Gly	Gly	Lys	Glu	Thr	Ala	Val		
785					790				795						800		
tcg	gtt	ttc	tat	cca	cgt	gaa	gac	atg	gta	gac	caa	ggg	tat	acc	acg		2448
Ser	Val	Phe	Tyr	Pro	Arg	Glu	Asp	Met	Val	Asp	Gln	Gly	Tyr	Thr	Thr		
				805					810					815			
ttt	ggg	tat	atg	aaa	atg	caa	atg	gtg	gta	gct	cat	ggg	gga	cgc	tgt		2496
Phe	Gly	Tyr	Met	Lys	Met	Gln	Met	Val	Val	Ala	His	Gly	Gly	Arg	Cys		
			820					825					830				
gct	gaa	cgt	gtg	gtt	ttt	ggc	gat	aat	gtc	act	gat	gga	gga	aaa	gat		2544
Ala	Glu	Arg	Val	Val	Phe	Gly	Asp	Asn	Val	Thr	Asp	Gly	Gly	Lys	Asp		
		835					840					845					
gac	ctg	gag	aag	ata	aca	aaa	att	gcc	agg	gag	atg	gtg	att	agc	cct		2592
Asp	Leu	Glu	Lys	Ile	Thr	Lys	Ile	Ala	Arg	Glu	Met	Val	Ile	Ser	Pro		
	850					855					860						
caa	agt	gcg	aga	tta	ggg	ctc	act	caa	ctt	gta	aaa	aag	att	gga	atg		2640
Gln	Ser	Ala	Arg	Leu	Gly	Leu	Thr	Gln	Leu	Val	Lys	Lys	Ile	Gly	Met		
865					870					875					880		
gtg	gat	tta	cca	gat	aac	cca	gac	ggc	gag	ctg	ata	aaa	tac	cgg	tgg		2688
Val	Asp	Leu	Pro	Asp	Asn	Pro	Asp	Gly	Glu	Leu	Ile	Lys	Tyr	Arg	Trp		
				885				890						895			
gac	cat	cct	cat	gta	atg	cca	gca	gag	atg	tcg	gta	gaa	gta	tcc	gag		2736
Asp	His	Pro	His	Val	Met	Pro	Ala	Glu	Met	Ser	Val	Glu	Val	Ser	Glu		
			900					905					910				
cta	ttc	acc	cgt	gag	ttg	aca	agg	tat	atc	gag	gag	act	gaa	gaa	ctt		2784
Leu	Phe	Thr	Arg	Glu	Leu	Thr	Arg	Tyr	Ile	Glu	Glu	Thr	Glu	Glu	Leu		
		915					920					925					
gcg	atg	aat	gct	ctg	aga	gca	aac	agg	cac	att	ctg	gac	tta	atc	acc		2832
Ala	Met	Asn	Ala	Leu	Arg	Ala	Asn	Arg	His	Ile	Leu	Asp	Leu	Ile	Thr		
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aga	gag	tta	tta	gaa	aaa	tca	agg	att	act	gga	ttg	gaa	gtg	gaa	gag		2880
Arg	Glu	Leu	Leu	Glu	Lys	Ser	Arg	Ile	Thr	Gly	Leu	Glu	Val	Glu	Glu		
945					950					955					960		
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Thr Val Pro Ser Phe Ile Asp Trp Asn Lys Trp Glu His Trp Lys Asp  
130 135 140

Ile Arg Asn Trp Asp Gly Lys Arg Val Ala Ala Leu Phe Ile Tyr Ala  
 145 150 155 160

Phe Ala Leu Leu Leu Ser Cys Gln Arg Val Tyr Val Ala Ile Gln Ala  
 165 170 175

Pro Arg Val Glu Arg Glu Arg Arg Glu Leu Thr Glu Ser Phe Met Glu  
 180 185 190

Ala Leu Ile Pro Glu Pro Ser Pro Gly Asn Ile Glu Lys Phe Lys Arg  
 195 200 205

Asn Met Trp Arg Lys Ala Thr Pro Lys Gly Leu Lys Leu Lys Arg Phe  
 210 215 220

Ile Glu Ala Pro Asp Gly Thr Leu Val His Asp Ser Ser Tyr Val Gly  
 225 230 235 240

Glu Asn Ala Trp Asp Asp Asp Leu Glu Thr Thr Glu Gly Ser Leu Lys  
 245 250 255

Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys  
 260 265 270

Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly  
 275 280 285

Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu  
 290 295 300

Lys Leu Ser Glu Gln Leu Asn Ser Ser Ala Ala Lys Tyr Val Val Glu  
 305 310 315 320

Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly  
 325 330 335

Arg Thr Ser Glu Thr Glu Gly Thr Arg Ala Leu Trp Ile Ser Lys Arg  
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Trp Trp Arg Tyr Arg Pro Lys Leu Pro Tyr Thr Tyr Phe Leu Gln Lys  
 355 360 365

Leu Asp Ser Ser Glu Val Ala Ala Val Val Phe Thr Glu Asp Leu Lys  
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Arg Leu Tyr Val Thr Met Lys Glu Gly Phe Pro Leu Glu Tyr Ile Val  
 385 390 395 400  
 Asp Ile Pro Leu Asp Pro Tyr Leu Phe Glu Thr Ile Cys Asn Ala Gly  
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 Val Glu Val Asp Leu Leu Gln Lys Arg Gln Ile His Tyr Phe Met Lys  
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 Pro Val Gly Asp Val Ser Glu Thr Lys Ser Met Tyr Lys Glu Val Val  
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 Ile Asp Ala Ile Ala Gly Arg His Ala Arg Lys Asp Pro Arg Arg Arg  
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Thr Gly Ile Asp Arg Phe Ser Leu Arg Gln Ala Val Ile Phe Ile Cys  
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Ala Thr Asn Arg Pro Asp Glu Leu Asp Leu Glu Phe Val Arg Ser Gly  
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Arg Ile Asp Arg Arg Leu Tyr Ile Gly Leu Pro Asp Ala Lys Gln Arg  
 660 665 670

Val Gln Ile Phe Gly Val His Ser Ala Gly Lys Asn Leu Ala Glu Asp  
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Ile Asp Phe Gly Lys Leu Val Phe Arg Thr Val Gly Phe Ser Gly Ala  
 690 695 700

Asp Ile Arg Asn Leu Val Asn Glu Ala Ala Ile Met Ser Val Arg Lys  
 705 710 715 720

Gly Arg Ser Tyr Ile Tyr Gln Gln Asp Ile Val Asp Val Leu Asp Lys  
 725 730 735

Gln Leu Leu Glu Gly Met Gly Val Leu Leu Thr Glu Glu Glu Gln Gln  
 740 745 750

Lys Cys Glu Gln Ser Val Ser Tyr Glu Lys Lys Arg Leu Leu Ala Val  
 755 760 765

His Glu Ala Gly His Ile Val Leu Ala His Leu Phe Pro Arg Phe Asp  
 770 775 780

Trp His Ala Phe Ser Gln Leu Leu Pro Gly Gly Lys Glu Thr Ala Val  
 785 790 795 800

Ser Val Phe Tyr Pro Arg Glu Asp Met Val Asp Gln Gly Tyr Thr Thr  
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Phe Gly Tyr Met Lys Met Gln Met Val Val Ala His Gly Gly Arg Cys  
 820 825 830

Ala Glu Arg Val Val Phe Gly Asp Asn Val Thr Asp Gly Gly Lys Asp  
 835 840 845

Asp Leu Glu Lys Ile Thr Lys Ile Ala Arg Glu Met Val Ile Ser Pro  
 850 855 860



Gln Ser Ala Arg Leu Gly Leu Thr Gln Leu Val Lys Lys Ile Gly Met  
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 Val Asp Leu Pro Asp Asn Pro Asp Gly Glu Leu Ile Lys Tyr Arg Trp  
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 Asp His Pro His Val Met Pro Ala Glu Met Ser Val Glu Val Ser Glu  
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Cys	Asp	Phe	Ser	Ser	Ser	Phe	Ser	Leu	Ala	Ser	Ser	Ser	Ser	Ser	Thr		
			20					25					30				
gtc	tcc	gtc	aca	acc	ttc	aac	att	tcc	tct	ctt	tcc	tct	aac	ccc	aac		144
Val	Ser	Val	Thr	Thr	Phe	Asn	Ile	Ser	Ser	Leu	Ser	Ser	Asn	Pro	Asn		
			35				40					45					
atc	atc	aat	tcc	agc	tca	act	ctc	ttc	cgt	tcc	ctt	tcc	ttc	tcc	ctt		192
Ile	Ile	Asn	Ser	Ser	Ser	Thr	Leu	Phe	Arg	Ser	Leu	Ser	Phe	Ser	Leu		
		50				55					60						
atc	cgc	cac	cgc	agc	agc	tac	tca	cgt	cgc	tct	ctc	cgc	cgt	ctc	tct		240
Ile	Arg	His	Arg	Ser	Ser	Tyr	Ser	Arg	Arg	Ser	Leu	Arg	Arg	Leu	Ser		
	65				70					75					80		
atc	cac	aca	gtt	cat	gga	aac	aaa	acc	caa	ttc	ttc	tct	cac	tcg	tct		288
Ile	His	Thr	Val	His	Gly	Asn	Lys	Thr	Gln	Phe	Phe	Ser	His	Ser	Ser		
				85					90					95			
aca	cga	act	cca	cca	ctt	ttc	acg	gct	aat	tcc	aca	gcc	caa	cga	agc		336
Thr	Arg	Thr	Pro	Pro	Leu	Phe	Thr	Ala	Asn	Ser	Thr	Ala	Gln	Arg	Ser		
			100					105					110				
ggg	act	ttc	gtc	gaa	cac	ctt	aca	ggc	att	aca	gaa	tcg	gaa	gaa	gga		384
Gly	Thr	Phe	Val	Glu	His	Leu	Thr	Gly	Ile	Thr	Glu	Ser	Glu	Glu	Gly		
		115					120					125					
atc	agc	gaa	gcc	aac	ggg	ttc	ggg	gat	gta	gag	tct	gct	agg	aac	gac		432
Ile	Ser	Glu	Ala	Asn	Gly	Phe	Gly	Asp	Val	Glu	Ser	Ala	Arg	Asn	Asp		
	130					135					140						
ata	aga	aac	gtc	gcg	act	cgt	aga	ata	gag	acg	gag	ttt	gaa	gtt	aga		480
Ile	Arg	Asn	Val	Ala	Thr	Arg	Arg	Ile	Glu	Thr	Glu	Phe	Glu	Val	Arg		
	145				150					155					160		
gaa	ttg	gaa	gag	ttg	cct	gag	gaa	tgg	cga	cgc	tcg	aag	cta	gct	tgg		528
Glu	Leu	Glu	Glu	Leu	Pro	Glu	Glu	Trp	Arg	Arg	Ser	Lys	Leu	Ala	Trp		
				165					170					175			
ctg	tgt	aaa	gag	gtt	cca	acg	cat	aag	gcc	gtg	acg	ctt	gtg	aga	ctc		576
Leu	Cys	Lys	Glu	Val	Pro	Thr	His	Lys	Ala	Val	Thr	Leu	Val	Arg	Leu		
			180					185					190				
ttg	aat	gct	cag	aag	aaa	tgg	gtt	cgt	caa	gag	gac	gct	act	tac	atc		624
Leu	Asn	Ala	Gln	Lys	Lys	Trp	Val	Arg	Gln	Glu	Asp	Ala	Thr	Tyr	Ile		
		195					200					205					
tct	gtt	cat	tgt	atg	cga	att	cgt	gag	aac	gaa	act	gga	ttc	agg	gtg		672
Ser	Val	His	Cys	Met	Arg	Ile	Arg	Glu	Asn	Glu	Thr	Gly	Phe	Arg	Val		
	210					215					220						
tat	aga	tgg	atg	aca	caa	cag	aat	tgg	tac	cgg	ttt	gat	ttc	ggg	tta		720
Tyr	Arg	Trp	Met	Thr	Gln	Gln	Asn	Trp	Tyr	Arg	Phe	Asp	Phe	Gly	Leu		
	225				230					235					240		
acg	acg	aag	cta	gct	gaa	tac	ttg	ggg	aaa	gaa	cgg	aaa	ttt	acg	aaa		768

Thr	Thr	Lys	Leu	Ala	Glu	Tyr	Leu	Gly	Lys	Glu	Arg	Lys	Phe	Thr	Lys		
				245					250					255			
tgt	cga	gag	gta	ttt	gat	gat	gtt	ttg	aat	caa	gga	cgt	gta	cca	agt		816
Cys	Arg	Glu	Val	Phe	Asp	Asp	Val	Leu	Asn	Gln	Gly	Arg	Val	Pro	Ser		
			260					265					270				
gaa	tct	aca	ttt	cat	att	ctt	gta	gtt	gcg	tat	cta	agt	agc	tta	tca		864
Glu	Ser	Thr	Phe	His	Ile	Leu	Val	Val	Ala	Tyr	Leu	Ser	Ser	Leu	Ser		
		275					280					285					
gta	gaa	ggg	tgt	ctc	gag	gaa	gcg	tgt	agt	gtt	tac	aat	aga	atg	att		912
Val	Glu	Gly	Cys	Leu	Glu	Glu	Ala	Cys	Ser	Val	Tyr	Asn	Arg	Met	Ile		
	290					295					300						
caa	ctt	gga	ggg	tac	aaa	ccg	cgt	ctt	agt	ctg	cat	aac	tct	ttg	ttt		960
Gln	Leu	Gly	Gly	Tyr	Lys	Pro	Arg	Leu	Ser	Leu	His	Asn	Ser	Leu	Phe		
305				310					315					320			
aga	gct	ttg	gtt	agt	aaa	caa	gga	ggg	att	ctg	aat	gat	cag	ctt	aag		1008
Arg	Ala	Leu	Val	Ser	Lys	Gln	Gly	Gly	Ile	Leu	Asn	Asp	Gln	Leu	Lys		
				325					330					335			
caa	gca	gag	ttt	atc	ttt	cac	aat	gtt	gtg	aca	acc	ggg	ctt	gag	gtt		1056
Gln	Ala	Glu	Phe	Ile	Phe	His	Asn	Val	Val	Thr	Thr	Gly	Leu	Glu	Val		
			340					345					350				
cag	aag	gat	att	tat	agt	gga	ttg	atc	tgg	ctg	cat	agt	tgt	caa	gat		1104
Gln	Lys	Asp	Ile	Tyr	Ser	Gly	Leu	Ile	Trp	Leu	His	Ser	Cys	Gln	Asp		
		355					360					365					
gaa	gtt	gat	ata	ggg	agg	ata	aac	tct	cta	aga	gaa	gag	atg	aag	aag		1152
Glu	Val	Asp	Ile	Gly	Arg	Ile	Asn	Ser	Leu	Arg	Glu	Glu	Met	Lys	Lys		
	370					375					380						
gcc	ggg	ttt	cag	gag	agt	aaa	gaa	gtt	gtg	gta	tcg	tta	ctt	aga	gct		1200
Ala	Gly	Phe	Gln	Glu	Ser	Lys	Glu	Val	Val	Val	Ser	Leu	Leu	Arg	Ala		
385					390					395				400			
tat	gca	aag	gag	gga	ggg	gtg	gaa	gaa	gtt	gag	agg	acg	tgg	ctt	gaa		1248
Tyr	Ala	Lys	Glu	Gly	Gly	Val	Glu	Glu	Val	Glu	Arg	Thr	Trp	Leu	Glu		
			405						410					415			
ttg	ctt	gat	tta	gat	tgt	ggg	ata	cct	tct	cag	gcg	ttt	gtg	tac	aaa		1296
Leu	Leu	Asp	Leu	Asp	Cys	Gly	Ile	Pro	Ser	Gln	Ala	Phe	Val	Tyr	Lys		
			420					425					430				
ata	gaa	gct	tat	tcg	aaa	gtc	ggc	gat	ttt	gcg	aaa	gct	atg	gag	ata		1344
Ile	Glu	Ala	Tyr	Ser	Lys	Val	Gly	Asp	Phe	Ala	Lys	Ala	Met	Glu	Ile		
		435					440					445					
ttt	agg	gag	atg	gag	aag	cat	ata	ggg	ggg	gca	act	atg	tct	gga	tac		1392
Phe	Arg	Glu	Met	Glu	Lys	His	Ile	Gly	Gly	Ala	Thr	Met	Ser	Gly	Tyr		
	450					455				460							
cat	aaa	atc	att	gag	gtt	cta	tgt	aaa	gtc	caa	caa	gtg	gaa	ctt	gtg		1440
His	Lys	Ile	Ile	Glu	Val	Leu	Cys	Lys	Val	Gln	Gln	Val	Glu	Leu	Val		
465					470				475				480				
gaa	act	ctc	atg	aag	gag	ttt	gaa	gaa	agc	ggg	aag	aag	ccg	ctt	cta		1488

Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu	485	490	495	
cca tca ttc atc gaa ata gcc aaa atg tac ttc gat ttg ggt tta cat				1536
Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His	500	505	510	
gag aaa ttg gag atg gct ttt gtt cag tgc ttg gag aaa tgc caa cct				1584
Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro	515	520	525	
agc cag cct ata tat aac ata tat ttg gat tca ttg act aaa ata ggc				1632
Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly	530	535	540	
aac ctt gag aaa gca ggg gat gtc ttc aat gaa atg aaa aac aac ggg				1680
Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly	545	550	555	560
aca atc aat gtg agt gct aga tcc tgc aac agc ctt tta aag gga tac				1728
Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr	565	570	575	
cta gat tgt gga aaa caa gtg cag gca gag aga ata tat gat ctg atg				1776
Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met	580	585	590	
aga atg aag aaa tac gaa atc gaa cca ccg ctt atg gaa aag ctt gat				1824
Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp	595	600	605	
tac atc ctg agc ttg aag aaa aaa gag gtg aag aag aga ccg ttt agc				1872
Tyr Ile Leu Ser Leu Lys Lys Lys Glu Val Lys Lys Arg Pro Phe Ser	610	615	620	
atg aag cta agc aaa gac cag cgt gag gta ttg gta ggt ttg ttg tta				1920
Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu	625	630	635	640
ggg ggc ttg caa atc gaa tca gac aaa gag aag aag agc cac atg atc				1968
Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile	645	650	655	
aaa ttt gaa ttt aga gaa aat tct caa gct cat ctg gtt ctt aaa caa				2016
Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln	660	665	670	
aac ata cat gac cag ttc cgt gag tgg ttg cat cct ttg agc aat ttt				2064
Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe	675	680	685	
cag gag gat att ata ccg ttc gaa ttc tac tcc gtt ccc cat tca tac				2112
Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr	690	695	700	
ttc ggg ttt tac gct gaa cat tac tgg cca aag ggt cag cca gag att				2160
Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile	705	710	715	720
cca aaa ctg att cat cgg tgg cta tcg cca cac tca ctc gcg tat tgg				2208

Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp  
725 730 735

tac atg tac agc ggc gtt aaa aca tca tca gga gac att atc ttg aga 2256  
Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg  
740 745 750

ttg aag gga agt ctc gaa ggt gtt gag aaa gta gta aag gct ctt caa 2304  
Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln  
755 760 765

gcc aaa tct atg gaa tgt cga gtt aag aag aaa gga aaa gtc ttc tgg 2352  
Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Gly Lys Val Phe Trp  
770 775 780

att gga ctt cag gga aca aac tca gct ttg ttc tgg aaa cta ata gag 2400  
Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu  
785 790 795 800

cct cat gtg tta gag aac ttg aaa gag cat ttg aaa cct gct tct gaa 2448  
Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu  
805 810 815

tca ctg gac aat gtt aag gaa gca gaa gaa caa agc atc aac ttc aaa 2496  
Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys  
820 825 830

tca aac tct gat cac agt gac gat tgt gtc aat tca gaa gca cat ttt 2544  
Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe  
835 840 845

tac tga 2550  
Tyr

&lt;210&gt; 8

&lt;211&gt; 849

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 8

Met Thr Lys Ser Asn Gly His Asn Ala Thr Met Ile Val Thr Gly Ala  
1 5 10 15

Cys Asp Phe Ser Ser Ser Phe Ser Leu Ala Ser Ser Ser Ser Ser Thr  
20 25 30

Val Ser Val Thr Thr Phe Asn Ile Ser Ser Leu Ser Ser Asn Pro Asn  
35 40 45

Ile Ile Asn Ser Ser Ser Thr Leu Phe Arg Ser Leu Ser Phe Ser Leu  
 50 55 60

Ile Arg His Arg Ser Ser Tyr Ser Arg Arg Ser Leu Arg Arg Leu Ser  
 65 70 75 80

Ile His Thr Val His Gly Asn Lys Thr Gln Phe Phe Ser His Ser Ser  
 85 90 95

Thr Arg Thr Pro Pro Leu Phe Thr Ala Asn Ser Thr Ala Gln Arg Ser  
 100 105 110

Gly Thr Phe Val Glu His Leu Thr Gly Ile Thr Glu Ser Glu Glu Gly  
 115 120 125

Ile Ser Glu Ala Asn Gly Phe Gly Asp Val Glu Ser Ala Arg Asn Asp  
 130 135 140

Ile Arg Asn Val Ala Thr Arg Arg Ile Glu Thr Glu Phe Glu Val Arg  
 145 150 155 160

Glu Leu Glu Glu Leu Pro Glu Glu Trp Arg Arg Ser Lys Leu Ala Trp  
 165 170 175

Leu Cys Lys Glu Val Pro Thr His Lys Ala Val Thr Leu Val Arg Leu  
 180 185 190

Leu Asn Ala Gln Lys Lys Trp Val Arg Gln Glu Asp Ala Thr Tyr Ile  
 195 200 205

Ser Val His Cys Met Arg Ile Arg Glu Asn Glu Thr Gly Phe Arg Val  
 210 215 220

Tyr Arg Trp Met Thr Gln Gln Asn Trp Tyr Arg Phe Asp Phe Gly Leu  
 225 230 235 240

Thr Thr Lys Leu Ala Glu Tyr Leu Gly Lys Glu Arg Lys Phe Thr Lys  
 245 250 255

Cys Arg Glu Val Phe Asp Asp Val Leu Asn Gln Gly Arg Val Pro Ser  
 260 265 270

Glu Ser Thr Phe His Ile Leu Val Val Ala Tyr Leu Ser Ser Leu Ser  
 275 280 285

Val Glu Gly Cys Leu Glu Glu Ala Cys Ser Val Tyr Asn Arg Met Ile  
 290 295 300

Gln Leu Gly Gly Tyr Lys Pro Arg Leu Ser Leu His Asn Ser Leu Phe  
 305 310 315 320

Arg Ala Leu Val Ser Lys Gln Gly Gly Ile Leu Asn Asp Gln Leu Lys  
 325 330 335

Gln Ala Glu Phe Ile Phe His Asn Val Val Thr Thr Gly Leu Glu Val  
 340 345 350

Gln Lys Asp Ile Tyr Ser Gly Leu Ile Trp Leu His Ser Cys Gln Asp  
 355 360 365

Glu Val Asp Ile Gly Arg Ile Asn Ser Leu Arg Glu Glu Met Lys Lys  
 370 375 380

Ala Gly Phe Gln Glu Ser Lys Glu Val Val Val Ser Leu Leu Arg Ala  
 385 390 395 400

Tyr Ala Lys Glu Gly Gly Val Glu Glu Val Glu Arg Thr Trp Leu Glu  
 405 410 415

Leu Leu Asp Leu Asp Cys Gly Ile Pro Ser Gln Ala Phe Val Tyr Lys  
 420 425 430

Ile Glu Ala Tyr Ser Lys Val Gly Asp Phe Ala Lys Ala Met Glu Ile  
 435 440 445

Phe Arg Glu Met Glu Lys His Ile Gly Gly Ala Thr Met Ser Gly Tyr  
 450 455 460

His Lys Ile Ile Glu Val Leu Cys Lys Val Gln Gln Val Glu Leu Val  
 465 470 475 480

Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu  
 485 490 495

Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His  
 500 505 510

Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro  
 515 520 525

Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly  
530 535 540

Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly  
545 550 555 560

Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr  
565 570 575

Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met  
580 585 590

Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp  
595 600 605

Tyr Ile Leu Ser Leu Lys Lys Lys Glu Val Lys Lys Arg Pro Phe Ser  
610 615 620

Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu  
625 630 635 640

Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile  
645 650 655

Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln  
660 665 670

Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe  
675 680 685

Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr  
690 695 700

Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile  
705 710 715 720

Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp  
725 730 735

Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg  
740 745 750

Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln  
755 760 765



Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Gly Lys Val Phe Trp  
 770 775 780

Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu  
 785 790 795 800

Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu  
 805 810 815

Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys  
 820 825 830

Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe  
 835 840 845

Tyr

<210> 9

<211> 1449

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1449)

<223> 8794

<400> 9

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Met Val Gly Ser Leu Glu Ser Asp Gln Thr Leu Ser Met Ala Thr Leu	
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atc gaa aaa ctc gac atc tta tct gac gac ttc gat cca acc gcc gta	96
Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val	
20 25 30	

gtc acc gaa ccg tta cct cct ccg gta act aat gga atc gga gct gat	144
Val Thr Glu Pro Leu Pro Pro Pro Val Thr Asn Gly Ile Gly Ala Asp	
35 40 45	

aaa gga gga gga gga gga gaa aga gag atg gtt ctc ggt agg aat ata	192
Lys Gly Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile	
50 55 60	

cac aca acg tca ctc gct gta acg gaa ccg gag gtt aac gat gaa ttc	240
His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe	
65 70 75 80	
acc gga gat aaa gaa gct tat atg gct agt gtt ctt gct cgt tac cgg	288
Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg	
85 90 95	
aaa act ttg gtt gaa cga acc aaa aac cat tta ggt tat cct tat aac	336
Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn	
100 105 110	
ttg gat ttc gac tat ggt gcg ctt ggt cag tta caa cat ttt tcg att	384
Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile	
115 120 125	
aat aat ctt gga gat ccg ttt att gaa agt aac tat ggt gta cac tca	432
Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser	
130 135 140	
aga cct ttt gaa gtt ggt gtg ttg gat tgg ttt gct cgt ctt tgg gag	480
Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu	
145 150 155 160	
att gag aga gat gat tat tgg ggt tac att acc aat tgt ggt act gaa	528
Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu	
165 170 175	
ggc aac ctt cat ggc att tta gtc ggg agg gag atg ttt ccg gat ggg	576
Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly	
180 185 190	
ata ttg tat gcg tcg cgt gaa tcg cat tac tcg gtg ttt aaa gct gct	624
Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala	
195 200 205	
cga atg tat cga atg gag tgt gag aag gtt gat acg ctt atg tca ggg	672
Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly	
210 215 220	
gag att gat tgt gat gat ttg agg aag aag ttg ttg gct aat aaa gat	720
Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Leu Ala Asn Lys Asp	
225 230 235 240	
aaa ccg gcg att ctt aat gtt aac ata gga acg acg gtt aaa gga gct	768
Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala	
245 250 255	
gtt gat gat ctt gac ctt gtt atc aaa act ctt gaa gag tgt ggt ttc	816
Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe	
260 265 270	
tca cat gat agg ttc tat att cat tgt gat gga gct ttg ttt gga ctt	864
Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu	
275 280 285	
atg atg cct ttt gtc aaa cgt gca ccg aaa gtg acg ttt aat aaa ccg	912
Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro	
290 295 300	

ata ggg agt gtg agt gta tcg ggc cac aaa ttt gtc ggg tgt cca atg 960  
 Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met  
 305 310 315 320

cca tgt ggt gtt cag ata aca aga atg gaa cat atc aaa gtc ctc tcc 1008  
 Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser  
 325 330 335

agt aac gtt gag tac ctt gct tca agg gat gca aca atc atg gga agt 1056  
 Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser  
 340 345 350

cgt aac ggg cat gct cct ttg ttc ctc tgg tac acc tta aac agg aaa 1104  
 Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys  
 355 360 365

ggt tac aaa gga ttc cag aaa gaa gtt cag aaa tgc ttg aga aac gcg 1152  
 Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala  
 370 375 380

cat tac ctc aaa gac cga ctt cgt gaa gct ggg att agc gcc atg ctt 1200  
 His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu  
 385 390 395 400

aat gag ctt agc agc act gtg gtc ttt gaa cgg cct aaa gat gaa gag 1248  
 Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu  
 405 410 415

ttt gtt aga agg tgg cag ctt gct tgc caa ggt gat ata gct cat gtg 1296  
 Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val  
 420 425 430

gtg gtt atg cca agt gtt aca atc gag aag ctt gat aat ttc ctg aaa 1344  
 Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys  
 435 440 445

gac ctt gtc aaa cac aga ttg atc tgg tac gag gat gga tct cag cct 1392  
 Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro  
 450 455 460

cct tgc ctt gca tcg gag gta gga acc aac aac tgc atc tgt cca gct 1440  
 Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala  
 465 470 475 480

cac aag tga 1449  
 His Lys

&lt;210&gt; 10

&lt;211&gt; 482

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 10

Met Val Gly Ser Leu Glu Ser Asp Gln Thr Leu Ser Met Ala Thr Leu  
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 Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val  
 20 25 30  
 Val Thr Glu Pro Leu Pro Pro Pro Val Thr Asn Gly Ile Gly Ala Asp  
 35 40 45  
 Lys Gly Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile  
 50 55 60  
 His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe  
 65 70 75 80  
 Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg  
 85 90 95  
 Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn  
 100 105 110  
 Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile  
 115 120 125  
 Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser  
 130 135 140  
 Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu  
 145 150 155 160  
 Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu  
 165 170 175  
 Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly  
 180 185 190  
 Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala  
 195 200 205  
 Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly  
 210 215 220  
 Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Leu Ala Asn Lys Asp  
 225 230 235 240

Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala  
                     245                    250                    255

Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe  
                     260                    265                    270

Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu  
                     275                    280                    285

Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro  
                     290                    295                    300

Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met  
 305                    310                    315                    320

Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser  
                     325                    330                    335

Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser  
                     340                    345                    350

Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys  
                     355                    360                    365

Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala  
                     370                    375                    380

His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu  
 385                    390                    395                    400

Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu  
                     405                    410                    415

Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val  
                     420                    425                    430

Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys  
                     435                    440                    445

Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro  
                     450                    455                    460

Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala  
 465                    470                    475                    480

His Lys

&lt;210&gt; 11

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(483)

&lt;223&gt; 9106

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<400> 11
atg gcg gaa cag act gag aaa gct ttt ctt aag cag cct aag gtc ttc      48
Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe
1          5          10          15

ctt agc tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga      96
Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
          20          25          30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa      144
Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
          35          40          45

gcc att gat gga gct tac gtt gac aag aaa tgc ccc ttc act gga act      192
Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr
          50          55          60

gtt tcc att aga ggt cgt atc tta gct ggt act tgc cac agt gcg aaa      240
Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys
65          70          75          80

atg cag agg acc att atc gtg cga agg gat tac ctt cac ttt gtg aag      288
Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys
          85          90          95

aag tat cag agg tat gag aag agg cat tca aac att ccg gct cat gtc      336
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val
          100          105          110

tca cca tgc ttc cgt gtt aag gaa gga gac cat atc atc att ggc caa      384
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln
          115          120          125

tgc agg cca ttg tcg aag aca gtg agg ttc aat gtg ttg aag gtg ata      432

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Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Ile  
 130 135 140  
 cca gct ggg tct tct tct tca ttt gga aag aag gca ttc act gga atg 480  
 Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly Met  
 145 150 155 160  
 taa 483

&lt;210&gt; 12

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 12

Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe  
 1 5 10 15

Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly  
 20 25 30

Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
 35 40 45

Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr  
 50 55 60

Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys  
 65 70 75 80

Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys  
 85 90 95

Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val  
 100 105 110

Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln  
 115 120 125

Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Ile  
 130 135 140

Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly Met  
 145 150 155 160

&lt;210&gt; 13

&lt;211&gt; 1170

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1170)

&lt;223&gt; 10708

&lt;400&gt; 13

atg tct cac agg aag ttt gag cac cca aga cat ggt tct ctt ggt ttc	48
Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe	
1 5 10 15	
ctt cca agg aag aga gct aac cgt cac aga gga aag gtg aag gcg ttc	96
Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe	
20 25 30	
cct aag gat gac caa acc aag cct tgc aag ttc aca gct ttc atg ggt	144
Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly	
35 40 45	
tac aaa gct ggt atg act cac att gtc aga gaa gtg gag aaa cct gga	192
Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly	
50 55 60	
tcc aag ctt cac aag aag gag aca tgt gag gct gtt acc atc att gag	240
Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu	
65 70 75 80	
aca cct gct atg gtg gtt gtt gga gtt gtt gcc tat gtg aag act cct	288
Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro	
85 90 95	
aga ggt ttg agg tct ttg aac act gtc tgg gca cag cat ttg agt gag	336
Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu	
100 105 110	
gag gtc agg aga agg ttc tac aag aac tgg gct aag tct aag aag aag	384
Glu Val Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys	
115 120 125	
gct ttc act ggg tac gct aag cag tat gac agt gag gat ggc aag aag	432
Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys	
130 135 140	
ggg att cag gct cag ctt gag aag atg aag aag tac gct act gtc atc	480



Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile 145 150 155 160	
cgt gtt ttg gct cac act cag atc agg aag atg aag gga ttg aag cag Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln 165 170 175	528
aag aag gct cac atg atg gag atc cag atc aat ggt ggt acc att gcc Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala 180 185 190	576
cag aag gtt gac ttt gcc tac agt ttc ttt gag aag cag atc cca att Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile 195 200 205	624
gaa gct gtc ttc cag aag gat gaa atg att gat atc att ggt gtg acc Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr 210 215 220	672
aag ggt aag ggt tat gaa ggt gtt gtt act cgt tgg ggt gtt acc cgt Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg 225 230 235 240	720
ctt cct cgt aag act cac aga ggt ctg cgt aag gtt gct tgt att ggt Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly 245 250 255	768
gcg tgg cat cct gct aga gtg tcc tac act gtt gct agg gct ggt cag Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln 260 265 270	816
aac ggt tac cat cac cgt act gag ctt aac aag aag att tac agg ttg Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu 275 280 285	864
ggt aag gtt ggt act gag gca cac aca gcc atg act gaa tat gac agg Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg 290 295 300	912
act gag aag gat gtg act cca atg gga ggc ttc cca cac tac ggt att Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile 305 310 315 320	960
gtg aag gat gac tac ttg atg att aag ggg tgc tgt gtt ggt ccc aag Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys 325 330 335	1008
aag aga gtt gta act ctc aga cag tca ctt ctc act cag act tcc cgt Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg 340 345 350	1056
ctt gcc ttg gag gag atc aaa ctc aag ttt att gac acc gcc tcc att Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile 355 360 365	1104
ttt gga cat ggt cgc ttc cag acc tcc ctt gag aag atg agg ttt tac Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr 370 375 380	1152
aac cgt gtc acg aag taa	1170

Asn Arg Val Thr Lys  
385

<210> 14

<211> 389

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe  
1 5 10 15

Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe  
20 25 30

Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly  
35 40 45

Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly  
50 55 60

Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu  
65 70 75 80

Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro  
85 90 95

Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu  
100 105 110

Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys  
115 120 125

Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys  
130 135 140

Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile  
145 150 155 160

Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln  
165 170 175

Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala  
 180 185 190

Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile  
 195 200 205

Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr  
 210 215 220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg  
 225 230 235 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly  
 245 250 255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln  
 260 265 270

Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu  
 275 280 285

Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg  
 290 295 300

Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile  
 305 310 315 320

Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys  
 325 330 335

Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg  
 340 345 350

Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile  
 355 360 365

Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr  
 370 375 380

Asn Arg Val Thr Lys  
 385

<210> 15

<211> 351

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(351)

&lt;223&gt; 10844

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<400> 15
atg aag cca gtg ata ggc aca gtg gta tcg aac aag atg caa aaa tct      48
Met Lys Pro Val Ile Gly Thr Val Val Ser Asn Lys Met Gln Lys Ser
1                               5                               10                               15

gta gtg gtc gcc gtc gat aga ctc ttc cac aac aaa atc tac aat cgc      96
Val Val Val Ala Val Asp Arg Leu Phe His Asn Lys Ile Tyr Asn Arg
                20                               25                               30

tac gtc aaa cga act tcc aaa ttc atg gct cac gac gac aaa gac gcc      144
Tyr Val Lys Arg Thr Ser Lys Phe Met Ala His Asp Asp Lys Asp Ala
                35                               40                               45

tgc aac atc ggc gat cga gtg aag tta gat cca tca agg cct ttg agc      192
Cys Asn Ile Gly Asp Arg Val Lys Leu Asp Pro Ser Arg Pro Leu Ser
                50                               55                               60

aag aat aag cat tgg att gtt gca gaa atc atc aaa aaa gct cga att      240
Lys Asn Lys His Trp Ile Val Ala Glu Ile Ile Lys Lys Ala Arg Ile
65                               70                               75                               80

tat tct cct aaa gct gct gct gct gct gtt tct gct tct gct tct gct      288
Tyr Ser Pro Lys Ala Ala Ala Ala Ala Val Ser Ala Ser Ala Ser Ala
                85                               90                               95

tcc tca gcc tcc act act gac tct tct gct cag tct cag att cct cca      336
Ser Ser Ala Ser Thr Thr Asp Ser Ser Ala Gln Ser Gln Ile Pro Pro
                100                               105                               110

tca tct act tct taa
Ser Ser Thr Ser
                115

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&lt;210&gt; 16

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 16

Met Lys Pro Val Ile Gly Thr Val Val Ser Asn Lys Met Gln Lys Ser  
 1 5 10 15

Val Val Val Ala Val Asp Arg Leu Phe His Asn Lys Ile Tyr Asn Arg  
 20 25 30

Tyr Val Lys Arg Thr Ser Lys Phe Met Ala His Asp Asp Lys Asp Ala  
 35 40 45

Cys Asn Ile Gly Asp Arg Val Lys Leu Asp Pro Ser Arg Pro Leu Ser  
 50 55 60

Lys Asn Lys His Trp Ile Val Ala Glu Ile Ile Lys Lys Ala Arg Ile  
 65 70 75 80

Tyr Ser Pro Lys Ala Ala Ala Ala Ala Val Ser Ala Ser Ala Ser Ala  
 85 90 95

Ser Ser Ala Ser Thr Thr Asp Ser Ser Ala Gln Ser Gln Ile Pro Pro  
 100 105 110

Ser Ser Thr Ser  
 115

&lt;210&gt; 17

&lt;211&gt; 1269

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1269)

&lt;223&gt; 10951

&lt;400&gt; 17

atg tct tct tct gta gca gtg tta tgg gtt gct act tct tct cta aat 48  
 Met Ser Ser Ser Val Ala Val Leu Trp Val Ala Thr Ser Ser Leu Asn  
 1 5 10 15

cca gac cca atg aac aat tgt ggg ttg gta agg gtt cta gaa tct tct 96  
 Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser

20	25	30	
aga ctg ttc tct cct tgt cag aat cag aga cta aac aaa ggt aag aag			144
Arg Leu Phe Ser Pro Cys Gln Asn Gln Arg Leu Asn Lys Gly Lys Lys			
35	40	45	
aag cag ata cca act tgg agt tct tct ttt gta agg aac cga agt aga			192
Lys Gln Ile Pro Thr Trp Ser Ser Ser Phe Val Arg Asn Arg Ser Arg			
50	55	60	
aga att ggt gtt gtg tct tca agc tta gta gca agt cct tct gga gag			240
Arg Ile Gly Val Val Ser Ser Ser Leu Val Ala Ser Pro Ser Gly Glu			
65	70	75	80
ata gct ctt tca tct gaa gag aag gtt tac aat gtt gtg ttg aaa caa			288
Ile Ala Leu Ser Ser Glu Glu Lys Val Tyr Asn Val Val Leu Lys Gln			
85	90	95	
gct gct ttg gtg aac aaa cag cta agg tct tct tct tat gac ctt gat			336
Ala Ala Leu Val Asn Lys Gln Leu Arg Ser Ser Ser Tyr Asp Leu Asp			
100	105	110	
gtg aag aaa cca caa gat gtt gtt ctt cct ggg agt ttg agt ttg ttg			384
Val Lys Lys Pro Gln Asp Val Val Leu Pro Gly Ser Leu Ser Leu Leu			
115	120	125	
ggt gaa gct tat gat cga tgc ggt gaa gtt tgc gct gaa tat cct aag			432
Gly Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Pro Lys			
130	135	140	
acg ttt tat ctt gga act ttg ctt atg aca ccc gaa agg cga aag gcg			480
Thr Phe Tyr Leu Gly Thr Leu Leu Met Thr Pro Glu Arg Arg Lys Ala			
145	150	155	160
att tgg gca atc tac gtt tgg tgt aga aga act gat gaa ctt gtg gat			528
Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp			
165	170	175	
ggg cca aat gct tca cat ata act ccc atg gct tta gat aga tgg gaa			576
Gly Pro Asn Ala Ser His Ile Thr Pro Met Ala Leu Asp Arg Trp Glu			
180	185	190	
gca agg tta gaa gat ctt ttc cgt ggt cgt cct ttc gat atg ctt gat			624
Ala Arg Leu Glu Asp Leu Phe Arg Gly Arg Pro Phe Asp Met Leu Asp			
195	200	205	
gct gct ctc gct gat aca gtt gct aga tac ccg gtc gat att cag cca			672
Ala Ala Leu Ala Asp Thr Val Ala Arg Tyr Pro Val Asp Ile Gln Pro			
210	215	220	
ttt cga gac atg atc gaa gga atg aga atg gac ttg aag aaa tcg aga			720
Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Lys Lys Ser Arg			
225	230	235	240
tac cag aac ttc gat gat cta tac ctt tac tgc tac tac gtc gct gga			768
Tyr Gln Asn Phe Asp Asp Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly			
245	250	255	
acc gtc gga ttg atg agc gtt ccg gtt atg gga atc gat cct aag tcg			816
Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Asp Pro Lys Ser			

260	265	270	
aaa gca aca acc gaa agt gtt tac aac gct gcc ttg gcc ctt ggt ata			864
Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile			
275	280	285	
gcc aat cag ctt act aac ata ctc aga gac gta ggc gaa gat gcg aga			912
Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg			
290	295	300	
aga gga agg gtt tat ctg cct cag gat gaa ttg gct cag gct ggt ctt			960
Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu			
305	310	315	320
tca gat gaa gac ata ttc gcc gga aaa gta act gat aaa tgg aga aac			1008
Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn			
325	330	335	
ttc atg aaa atg cag ctt aaa cga gca aga atg ttc ttc gac gaa gct			1056
Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala			
340	345	350	
gag aaa ggc gtc acc gag ctc agt gcc gct agc aga tgg cct gta tgg			1104
Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp			
355	360	365	
gct tca ttg cta ttg tac agg aga ata ctg gac gag att gaa gcg aat			1152
Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn			
370	375	380	
gat tac aac aat ttt act aag aga gct tat gtg ggg aaa gtc aag aaa			1200
Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys			
385	390	395	400
att gca gct ttg cca ttg gct tat gct aaa tca gta cta aag act tca			1248
Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser			
405	410	415	
agt tca aga cta tcg ata tga			1269
Ser Ser Arg Leu Ser Ile			
420			

&lt;210&gt; 18

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 18

Met	Ser	Ser	Ser	Val	Ala	Val	Leu	Trp	Val	Ala	Thr	Ser	Ser	Leu	Asn
1				5					10					15	

Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser

20 25 30  
 Arg Leu Phe Ser Pro Cys Gln Asn Gln Arg Leu Asn Lys Gly Lys Lys  
 35 40 45  
 Lys Gln Ile Pro Thr Trp Ser Ser Ser Phe Val Arg Asn Arg Ser Arg  
 50 55 60  
 Arg Ile Gly Val Val Ser Ser Ser Leu Val Ala Ser Pro Ser Gly Glu  
 65 70 75 80  
 Ile Ala Leu Ser Ser Glu Glu Lys Val Tyr Asn Val Val Leu Lys Gln  
 85 90 95  
 Ala Ala Leu Val Asn Lys Gln Leu Arg Ser Ser Ser Tyr Asp Leu Asp  
 100 105 110  
 Val Lys Lys Pro Gln Asp Val Val Leu Pro Gly Ser Leu Ser Leu Leu  
 115 120 125  
 Gly Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Pro Lys  
 130 135 140  
 Thr Phe Tyr Leu Gly Thr Leu Leu Met Thr Pro Glu Arg Arg Lys Ala  
 145 150 155 160  
 Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp  
 165 170 175  
 Gly Pro Asn Ala Ser His Ile Thr Pro Met Ala Leu Asp Arg Trp Glu  
 180 185 190  
 Ala Arg Leu Glu Asp Leu Phe Arg Gly Arg Pro Phe Asp Met Leu Asp  
 195 200 205  
 Ala Ala Leu Ala Asp Thr Val Ala Arg Tyr Pro Val Asp Ile Gln Pro  
 210 215 220  
 Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Lys Lys Ser Arg  
 225 230 235 240  
 Tyr Gln Asn Phe Asp Asp Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly  
 245 250 255  
 Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Asp Pro Lys Ser



260	265	270
Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile		
275	280	285
Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg		
290	295	300
Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu		
305	310	315
Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn		
325	330	335
Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala		
340	345	350
Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp		
355	360	365
Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn		
370	375	380
Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys		
385	390	395
Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser		
405	410	415
Ser Ser Arg Leu Ser Ile		
420		

&lt;210&gt; 19

&lt;211&gt; 1125

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1125)

&lt;223&gt; 12935

&lt;400&gt; 19

atg gga gca gcg aag aat atc tgg gca tta gcc aac gcc gaa gat gca	48
Met Gly Ala Ala Lys Asn Ile Trp Ala Leu Ala Asn Ala Glu Asp Ala	
1 5 10 15	
gct aac gac gcc gaa caa atc cct tat tct tcg ttc gtc gtc gac acg	96
Ala Asn Asp Ala Glu Gln Ile Pro Tyr Ser Ser Phe Val Val Asp Thr	
20 25 30	
tct ttg cct ctt cct ctc atg att cct cgt atc ata gag tta tgt aaa	144
Ser Leu Pro Leu Pro Leu Met Ile Pro Arg Ile Ile Glu Leu Cys Lys	
35 40 45	
gat ctg ttc aag aat tgg gga gag ctt gat gat tca ctc ttc tct gtt	192
Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val	
50 55 60	
gag aga gta tct gga ggc att aca aat ctt ttg ctg aag gtt tct gtg	240
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**Published:**

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH

(57) Abstract: Nucleotide sequences are isolated from *Arabidopsis thaliana* that code for proteins essential for plant growth and development. The essentially of the proteins may be exploited by recombinantly expressing the proteins and using them in screening assays to identify compounds that interact with or inhibit the proteins and are therefore potential herbicides.

WO 2003/008440 A3

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 02/07929

**A. CLASSIFICATION OF SUBJECT MATTER**  
IPC 7 G01N33/68 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data, PAJ, Sequence Search, CHEM ABS Data

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] 1 March 2001 (2001-03-01), XP002253634 accession no. EBI Database accession no. Q9FKB8 abstract & KOTANI, H. ET AL: "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones." DNA RES., 1998, pages 203-216, the whole document	1-10
A	WO 00/42205 A (NOVARTIS ERFIND VERWALT GMBH ;NOVARTIS AG (CH); BUDZISZEWSKI GREGO) 20 July 2000 (2000-07-20) abstract; claims 39-44 ----- -/--	1-10

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

28 October 2003

Date of mailing of the international search report

20.01.04

Name and mailing address of the ISA

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Authorized officer

Luis Alves, D

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 02/07929

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; June 2001 (2001-06), WILLIAMS MARK A ET AL: "Characterization and inhibition of chloroplast-localized peptide deformylases from Arabidopsis thaliana" XP002253632 Database accession no. PREV200100419457 abstract &amp; HORTSCIENCE, vol. 36, no. 3, June 2001 (2001-06), page 554, 98th Annual International Conference of the American Society for Horticultural Science; Sacramento, California, USA; July 21-25, 2001 ISSN: 0018-5345</p>	1-10
A	<p>----- ITO TAKUYA ET AL: "Regional insertional mutagenesis of genes on Arabidopsis thaliana chromosome V using the Ac/Ds transposon in combination with a cDNA scanning method." PLANT JOURNAL, vol. 17, no. 4, February 1999 (1999-02), pages 433-444, XP002253633 ISSN: 0960-7412 the whole document</p>	1-10
A	<p>----- WO 00/15809 A (NOVARTIS ERFIND VERWALT GMBH ; NOVARTIS AG (CH); BUDZISZEWSKI GREGO) 23 March 2000 (2000-03-23) abstract page 8, paragraph 3 - page 17, last paragraph -----</p>	1-10

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/EP 02/07929

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see PCT/ISA/210 annex

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-10 (all partially)

Invention 1

Screening methods for herbicidal compounds comprising identifying ligands or inhibitors of the protein having SEQ Id No 2.

---

2. claims: 1-10 (all partially)

Inventions 2 to 48

Screening methods for herbicidal compounds comprising identifying ligands or inhibitors of the protein having SEQ Id No n (with n=4...96, n being an even number).

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# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 02/07929

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 0042205	A	20-07-2000	AU 2290900 A CA 2362484 A1 CN 1341151 T WO 0042205 A2 EP 1141344 A2 JP 2002534128 T	01-08-2000 20-07-2000 20-03-2002 20-07-2000 10-10-2001 15-10-2002
WO 0015809	A	23-03-2000	AU 6082399 A CA 2340332 A1 CN 1318106 T WO 0015809 A2 EP 1114168 A2 JP 2002525061 T	03-04-2000 23-03-2000 17-10-2001 23-03-2000 11-07-2001 13-08-2002

Form PCT/ISA/210 (patent family annex) (July 1992)



49

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 1 5 10 15

48

att gct tca ttc act gga aat gga gaa gct tct tct tct tcc tca gag  
 Ile Ala Ser Phe Thr Gly Asn Gly Glu Ala Ser Ser Ser Ser Ser Glu  
 20 25 30

96

aac aat ggc tgc aat gga gat caa aac cat ttg ctt aac gaa ctc aaa  
 Asn Asn Gly Cys Asn Gly Asp Gln Asn His Leu Leu Asn Glu Leu Lys  
 35 40 45

144

tcc acc gtc tct gct ctt caa tca atc atc aag gag aaa aac caa gaa Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu 50 55 60	192
ttg ctt agc aag gaa gag aaa atc cga ggt ttg gag tta tat atc agg Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg 65 70 75 80	240
gag aaa cct tat ttg ttt gag agt gaa att gat ttt tct caa ttt gag Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu 85 90 95	288
aat ccg gta aag cat gcg agt gaa gta gaa gag aag gtt tat gaa cta Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu 100 105 110	336
cag aaa cag gta ttt gga tta aaa cgg gaa gtg gaa acg caa cgc aag Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys 115 120 125	384
aga agg ctc gaa gtg gaa gct gaa tta gca gat aag aaa gtt gca caa Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln 130 135 140	432
ctt agc tca aag ctt gaa aat atc gat ggg tgg ttc ttg tct aaa ctt Leu Ser Ser Lys Leu Glu Asn Ile Asp Gly Trp Phe Leu Ser Lys Leu 145 150 155 160	480
ggg ctt aac ccg act gaa agt cag gca tat ctg atg acc cta tgg cat Gly Leu Asn Pro Thr Glu Ser Gln Ala Tyr Leu Met Thr Leu Trp His 165 170 175	528
caa cat ctt agc cca act ctt cat acc act ctt caa atg gtg tcg atg Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met 180 185 190	576
aaa att gag caa gtc cag aaa tgg tca gag cct cac att gaa aca ctg Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu 195 200 205	624
aac tca caa tgg att cca agc atc aaa gat gca tgt gtc aca ata acc Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr 210 215 220	672
ata tat ctc gaa cca aaa gtt caa tat ata acc gat aag tcc atc gag Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu 225 230 235 240	720
ttg tta tat aca tct aag cag gct ttg aca cca cat ctc atc caa gga Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly 245 250 255	768
ttt gac gct tca tac tac tat ctt gag gtg atc aga aca cat aca cat Phe Asp Ala Ser Tyr Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His 260 265 270	816
ccg tac acg acc cgg att atg acc tta acg aag cca cac ttg gag aga Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg 275 280 285	864

gta caa gtt gcc tta gag cca tat act gaa aac gta aga cat ggc ttt 912  
 Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe  
 290 295 300  
 cag aag ttg gtt aac tca acc aaa atc tac cat caa cag gct caa gaa 960  
 Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu  
 305 310 315 320  
 atg ctg aag aac aat gag atc acc aaa ccg gtt gct acc atg gac tta 1008  
 Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu  
 325 330 335  
 gct tgg gtt ggg gcc aca gct tta att gga ttc cct ctt ata ttc atc 1056  
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 340 345 350  
 atc aaa ttg ctt tct gca gtc tcc aat cct aag ggg aag aag aga cac 1104  
 Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His  
 355 360 365  
 aac cat aaa aaa gaa cca acc acc ggg tac cgc aga gcc aaa cgc cga 1152  
 Asn His Lys Lys Glu Pro Thr Thr Gly Tyr Arg Arg Ala Lys Arg Arg  
 370 375 380  
 cat cct cac caa tga 1167  
 His Pro His Gln  
 385

&lt;210&gt; 24

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 24

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 1 5 10 15

Ile Ala Ser Phe Thr Gly Asn Gly Glu Ala Ser Ser Ser Ser Ser Glu  
 20 25 30

Asn Asn Gly Cys Asn Gly Asp Gln Asn His Leu Leu Asn Glu Leu Lys  
 35 40 45

Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu  
 50 55 60

Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg  
 65 70 75 80



Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu  
                     85                                    90                                    95

Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu  
                     100                                    105                                    110

Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys  
                     115                                    120                                    125

Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln  
                     130                                    135                                    140

Leu Ser Ser Lys Leu Glu Asn Ile Asp Gly Trp Phe Leu Ser Lys Leu  
                     145                                    150                                    155                                    160

Gly Leu Asn Pro Thr Glu Ser Gln Ala Tyr Leu Met Thr Leu Trp His  
                     165                                    170                                    175

Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met  
                     180                                    185                                    190

Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu  
                     195                                    200                                    205

Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr  
                     210                                    215                                    220

Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu  
                     225                                    230                                    235                                    240

Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly  
                     245                                    250                                    255

Phe Asp Ala Ser Tyr Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His  
                     260                                    265                                    270

Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg  
                     275                                    280                                    285

Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe  
                     290                                    295                                    300

Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu  
                     305                                    310                                    315                                    320

Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu  
 325 330 335

Ala Trp Val Gly Ala Thr Ala Leu Ile Gly Phe Pro Leu Ile Phe Ile  
 340 345 350

Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His  
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Asn His Lys Lys Glu Pro Thr Thr Gly Tyr Arg Arg Ala Lys Arg Arg  
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His Pro His Gln  
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<211> 2463

<212> DNA

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<223> 14610.1

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1 5 10 15	
aat cgt aga tat ctg agt caa gtt atg gat acg tgc ggc aag gat tta	96
Asn Arg Arg Tyr Leu Ser Gln Val Met Asp Thr Cys Gly Lys Asp Leu	
20 25 30	
tct acg gcg gag gac atc gtt gat gat ctt cgt tcc agg tac ggc aat	144
Ser Thr Ala Glu Asp Ile Val Asp Asp Leu Arg Ser Arg Tyr Gly Asn	
35 40 45	
ttt gcg agg ttg act cgg caa gtg ctt cta ctc aat gtc agg caa gtc	192
Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Leu Asn Val Arg Gln Val	
50 55 60	
ctt aat gtt aga aac aac aag agg gtt aaa gac gaa gat gaa gat gac	240

Leu Asn Val Arg Asn Asn Lys Arg Val Lys Asp Glu Asp Glu Asp Asp	65	70	75	80
aac att gga gat gag gaa ggt tct gct tct cag agg aag aaa cag aga	288			
Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg		85	90	95
cgg gtt gat gag aaa gag gag aaa ttg cag cga gcg gag cag tcg cat	336			
Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His		100	105	110
tta agg aag agg aat atg gaa cgt tca gtg tct tct tct ccg tct tct	384			
Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Ser Pro Ser Ser		115	120	125
tct tct tct tcg gaa gac agt ggt gat gtg tcg act tct gag gac gcg	432			
Ser Ser Ser Ser Glu Asp Ser Gly Asp Val Ser Thr Ser Glu Asp Ala		130	135	140
gtt tat ggc gag aag ctg agt ccg ccg cgg ttt gat ctg atc aat gac	480			
Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp		145	150	155
agt cta aga gat aac tac gct aag ttg aac agc tcc tcg aag aaa cca	528			
Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro		165	170	175
att ggg tcg cct gcg gaa aag aat gtg gaa gtt gag act gtg agc aac	576			
Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn		180	185	190
aaa ggt aga agc aag ttg gct aca atg ggg gcc aga aag gag gct aaa	624			
Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys		195	200	205
gtt tct ctt tcc ctc agt gga gct act ggt aat ggt gat ttg gaa gtt	672			
Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val		210	215	220
gag ggt act aaa gga cct act ttt aaa gac ttt ggt ggg att aag aaa	720			
Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys		225	230	235
ata ttg gat gaa ttg gag atg aat gtt cta ttc ccc att ctc aat cct	768			
Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro		245	250	255
gag ccg ttt aag aag att gga gtg aag cca cca agt ggg att cta ttt	816			
Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe		260	265	270
cat gga cca cct ggc tgt ggg aag act aag ttg gcc aat gcc att gcc	864			
His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala		275	280	285
aat gaa gct ggt gtt ccg ttt tat aag att tca gcc aca gag gtg att	912			
Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile		290	295	300
tct ggt gtt tct ggt gct tct gaa gag aat atc aga gag ctc ttt tct	960			

Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser  
 305 310 315 320  
 1008  
 aaa gca tat agg act gcg cct tcg att gtg ttt atc gat gag att gat  
 Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp  
 325 330 335  
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 gcg att ggt tca aag aga gag aat cag caa aga gag atg gag aag cgg  
 Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg  
 340 345 350  
 1104  
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 Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly  
 355 360 365  
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 gat aaa aat gct cct gat tct agt gct ggt ttt gtt ctt gtc att gga  
 Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly  
 370 375 380  
 1200  
 gct aca aat agg cct gat gct ctt gat cct gct ttg agg aga agt gga  
 Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly  
 385 390 395 400  
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 cga ttt gaa act gag atc gct cta act gct cca gat gaa gac gca agg  
 Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg  
 405 410 415  
 1296  
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 Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro  
 420 425 430  
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 Phe Asp Lys Lys Arg Ile Ala Arg Leu Thr Pro Gly Phe Val Gly Ala  
 435 440 445  
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 Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg  
 450 455 460  
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 Ile Leu Asp Ser Arg Lys Ser Glu Gln Ser Gly Asp Gly Glu Asp Asp  
 465 470 475 480  
 1488  
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 Lys Ser Trp Leu Arg Met Pro Trp Pro Glu Glu Glu Leu Glu Lys Leu  
 485 490 495  
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 500 505 510  
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 Ser Leu Thr Arg Glu Gly Phe Ser Ile Val Pro Asp Val Lys Trp Asp  
 515 520 525  
 1632  
 gat gtt ggt gga ctt gac cat cta cga ctt caa ttc aac cgt tat ata  
 Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile  
 530 535 540  
 1680  
 gtg agg cct atc aaa aag cct gat att tat aag gct ttt ggg gta gac

61

Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu  
785 790 795 800

caa gaa agc gtt ggg agg aac act gaa caa gtc acc ata ggg cca tct 2448  
Gln Glu Ser Val Gly Arg Asn Thr Glu Gln Val Thr Ile Gly Pro Ser 815

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Phe Thr Leu Glu 820

<210> 26

<211> 820

<212> PRT

<213> Arabidopsis thaliana

<400> 26

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20 25 30

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35 40 45

Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Leu Asn Val Arg Gln Val  
50 55 60

Leu Asn Val Arg Asn Asn Lys Arg Val Lys Asp Glu Asp Glu Asp Asp  
65 70 75 80

Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg  
85 90 95

Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His  
100 105 110

Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Ser Pro Ser Ser  
115 120 125

Ser Ser Ser Ser Glu Asp Ser Gly Asp Val Ser Thr Ser Glu Asp Ala  
130 135 140

Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp  
 145 150 155 160

Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro  
 165 170 175

Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn  
 180 185 190

Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys  
 195 200 205

Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val  
 210 215 220

Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys  
 225 230 235 240

Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro  
 245 250 255

Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe  
 260 265 270

His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala  
 275 280 285

Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile  
 290 295 300

Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser  
 305 310 315 320

Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp  
 325 330 335

Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg  
 340 345 350

Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly  
 355 360 365

Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly  
 370 375 380

Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly  
 385 390 395 400

Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg  
 405 410 415

Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro  
 420 425 430

Phe Asp Lys Lys Arg Ile Ala Arg Leu Thr Pro Gly Phe Val Gly Ala  
 435 440 445

Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg  
 450 455 460

Ile Leu Asp Ser Arg Lys Ser Glu Gln Ser Gly Asp Gly Glu Asp Asp  
 465 470 475 480

Lys Ser Trp Leu Arg Met Pro Trp Pro Glu Glu Glu Leu Glu Lys Leu  
 485 490 495

Phe Val Lys Met Ser Asp Phe Glu Glu Ala Val Asn Leu Val Gln Ala  
 500 505 510

Ser Leu Thr Arg Glu Gly Phe Ser Ile Val Pro Asp Val Lys Trp Asp  
 515 520 525

Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile  
 530 535 540

Val Arg Pro Ile Lys Lys Pro Asp Ile Tyr Lys Ala Phe Gly Val Asp  
 545 550 555 560

Leu Glu Thr Gly Phe Leu Leu Tyr Gly Pro Pro Gly Cys Gly Lys Thr  
 565 570 575

Leu Ile Ala Lys Ala Ala Ala Asn Glu Ala Gly Ala Asn Phe Met His  
 580 585 590

Ile Lys Gly Ala Glu Leu Leu Asn Lys Tyr Val Gly Glu Ser Glu Leu  
 595 600 605

Ala Ile Arg Thr Leu Phe Gln Arg Ala Arg Thr Cys Ala Pro Cys Val  
 610 615 620



Ile Phe Phe Asp Glu Val Asp Ala Leu Thr Thr Ser Arg Gly Lys Glu  
625 630 635 640

Gly Ala Trp Val Val Glu Arg Leu Leu Asn Gln Phe Leu Val Glu Leu  
645 650 655

Asp Gly Gly Glu Arg Arg Asn Val Tyr Val Ile Gly Ala Thr Asn Arg  
660 665 670

Pro Asp Val Val Asp Pro Ala Phe Leu Arg Pro Gly Arg Phe Gly Asn  
675 680 685

Leu Leu Tyr Val Pro Leu Pro Asn Ala Asp Glu Arg Ala Ser Ile Leu  
690 695 700

Lys Ala Ile Ala Arg Lys Lys Pro Ile Asp Pro Ser Val Asp Leu Asp  
705 710 715 720

Gly Ile Ala Lys Asn Asn Cys Glu Gly Phe Ser Gly Ala Asp Leu Ala  
725 730 735

His Leu Val Gln Lys Ala Thr Phe Gln Ala Val Glu Glu Met Ile Gly  
740 745 750

Ser Ser Glu Ser Ser Glu Asp Asp Val Thr Asp Ile Thr Gln Cys Thr  
755 760 765

Ile Lys Thr Arg His Phe Glu Gln Ala Leu Ser Leu Val Ser Pro Ser  
770 775 780

Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu  
785 790 795 800

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Phe Thr Leu Glu  
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<211> 1002

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&lt;223&gt; 14891

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1          5          10          15

ggg ttc gat gat ccg agt atc gac aag atg ttg aga aaa tgc aaa cag      96
Gly Phe Asp Asp Pro Ser Ile Asp Lys Met Leu Arg Lys Cys Lys Gln
          20          25          30

ttg gaa aag gct caa agc gat gtg gca tca gaa aac tgg gac tac ctg      144
Leu Glu Lys Ala Gln Ser Asp Val Ala Ser Glu Asn Trp Asp Tyr Leu
          35          40          45

agt aac att gtt ggt atc caa gag aga aaa ctc cct tac atc gtc tct      192
Ser Asn Ile Val Gly Ile Gln Glu Arg Lys Leu Pro Tyr Ile Val Ser
          50          55          60

cga tgc ccc aaa atc ctg act tta cgc ctc gat gag aga ctc atc ccg      240
Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro
65          70          75          80

atg gtc gag tgc ctc tcc agt ctt gga agg aat cct cgg gaa gtt gct      288
Met Val Glu Cys Leu Ser Ser Leu Gly Arg Asn Pro Arg Glu Val Ala
          85          90          95

tcc gcc att acc aaa ttt cct cca ata ctc tct cat agc gtg gag gag      336
Ser Ala Ile Thr Lys Phe Pro Pro Ile Leu Ser His Ser Val Glu Glu
          100          105          110

aaa ctc tgt ccc ctt ctt gct ttc ttt caa gcg tta ggt gtg cct gag      384
Lys Leu Cys Pro Leu Leu Ala Phe Phe Gln Ala Leu Gly Val Pro Glu
          115          120          125

act caa ctt ggc aaa atg ata ctt ttt aac cca agg ctt atc agc tac      432
Thr Gln Leu Gly Lys Met Ile Leu Phe Asn Pro Arg Leu Ile Ser Tyr
          130          135          140

agc atc gac acc aag ctg aca gtg atc gtc agc ttt ctt gct agc ctt      480
Ser Ile Asp Thr Lys Leu Thr Val Ile Val Ser Phe Leu Ala Ser Leu
145          150          155          160

ggc ctt gat caa gat ggg atg att ggc aaa gtt ttg gtg aag aac cca      528
Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro
          165          170          175

ttt ctt atg ggg tac agt gtt gat aaa agg tta cgg cct acc act gaa      576
Phe Leu Met Gly Tyr Ser Val Asp Lys Arg Leu Arg Pro Thr Thr Glu
          180          185          190

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 210 215 220  
  
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 Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln  
 225 230 235 240  
  
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 Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val  
 245 250 255  
  
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 290 295 300  
  
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 Ile Asp Cys Ser Leu Arg Glu Met Leu Asp Cys Asn Thr Lys Lys Phe  
 305 310 315 320  
  
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 325 330

&lt;210&gt; 28

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 28

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Gly Phe Asp Asp Pro Ser Ile Asp Lys Met Leu Arg Lys Cys Lys Gln  
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Leu Glu Lys Ala Gln Ser Asp Val Ala Ser Glu Asn Trp Asp Tyr Leu  
 35 40 45

Ser Asn Ile Val Gly Ile Gln Glu Arg Lys Leu Pro Tyr Ile Val Ser  
 50 55 60

Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro  
 65 70 75 80

Met Val Glu Cys Leu Ser Ser Leu Gly Arg Asn Pro Arg Glu Val Ala  
 85 90 95

Ser Ala Ile Thr Lys Phe Pro Pro Ile Leu Ser His Ser Val Glu Glu  
 100 105 110

Lys Leu Cys Pro Leu Leu Ala Phe Phe Gln Ala Leu Gly Val Pro Glu  
 115 120 125

Thr Gln Leu Gly Lys Met Ile Leu Phe Asn Pro Arg Leu Ile Ser Tyr  
 130 135 140

Ser Ile Asp Thr Lys Leu Thr Val Ile Val Ser Phe Leu Ala Ser Leu  
 145 150 155 160

Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro  
 165 170 175

Phe Leu Met Gly Tyr Ser Val Asp Lys Arg Leu Arg Pro Thr Thr Glu  
 180 185 190

Phe Leu Lys Ser Ser Val Gly Leu Ser Glu Asp Gly Ile Lys Ser Val  
 195 200 205

Val Met Asn Phe Pro Gln Leu Leu Cys Arg Asp Val Asn Lys Ile Leu  
 210 215 220

Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln  
 225 230 235 240

Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val  
 245 250 255

Lys Asn Ser Leu Gln Pro Arg Ile Arg Phe Leu Val Gln Val Met Gly  
 260 265 270

Arg Gly Met Asp Glu Val Ala Ser Tyr Pro Glu Phe Phe His His Gly  
 275 280 285

Leu Lys Lys Lys Val Glu Ser Arg Phe Lys Leu Val Lys Lys Asn Asn  
 290 295 300

Ile Asp Cys Ser Leu Arg Glu Met Leu Asp Cys Asn Thr Lys Lys Phe  
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<212> DNA

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<223> 14986

<400> 29

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 1 5 10 15

act cat cgc atc tac aag cat gag tgt tgc atc tcc ttc gat act ccg 96  
 Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro  
 20 25 30

aga tcc gaa gga gga ttg ttc gtt gat atg aat agt ttt ctt gct ttc 144  
 Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe  
 35 40 45

ggg aag gat tat gtt tct tgg aac tat gag aag act gga aac cct gtt 192  
 Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val  
 50 55 60

tat ctt cat att aag cag act agg aag tct att ccc gag gat cgg cct 240  
 Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro  
 65 70 75 80

ctc aag aaa ccg act ctg ctc gct ata ggt gtt gat gga ggc ttt gat 288  
 Leu Lys Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Gly Phe Asp  
 85 90 95

aac aat gag cca gag tac gag gag tct tat agc ata gtc ata ctt ccg 336

Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro	
100 105 110	
gat ttt gtt tca ctc ccg ttt cct tct gtt gag cta cca gag aag gtg	384
Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val	
115 120 125	
agg att gct gtc gat act gta gtg aat gcc gtt ggt gct gag cgg aaa	432
Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys	
130 135 140	
gag caa gtt gca gct tgg aca gct gag aaa aag tta att agt gaa cat	480
Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His	
145 150 155 160	
gca ttg aca ctg cag caa atc aag agt ggc att gtc att cct ccc tct	528
Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser	
165 170 175	
ggt tgg aaa tgt tct aag tgt gat aag acg gag aat ctc tgg ctt aat	576
Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn	
180 185 190	
ctt acc gat gga atg att ctc tgt gga aga aaa aac tgg gat gga act	624
Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr	
195 200 205	
ggt gga aac aac cat gct gtt gag cac tac aaa gag aca gcc tac cct	672
Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro	
210 215 220	
ctt gct gta aag ctt gga act atc act gct gac tta gaa gca gca gat	720
Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp	
225 230 235 240	
gtt tat tcc tat ccg gaa gat gac agt gtt ttg gac ccg ctc ctg gct	768
Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala	
245 250 255	
gag cat ctg gcc cat ttt gga att gac ttc tcg tcg atg cag aag act	816
Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr	
260 265 270	
gaa atg aca act gct gaa aga gaa ctt gat caa aat aca aat ttt gat	864
Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp	
275 280 285	
tgg aac cgt ata caa gag agt gga aaa gaa ttg gtg cca gtt ttt gga	912
Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly	
290 295 300	
cct gga tat acc gga ctt gtc aat ctt ggg aac agt tgc tac ttg gca	960
Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala	
305 310 315 320	
gct acg atg cag att gtt ttc tct acc cat tca ttt att tca aga tac	1008
Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr	
325 330 335	
ttt tca cat cag agc tta aag atg gct ttt gag atg gct cct gct gat	1056

Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp	
340 345 350	
cca act ttg gac ctc aat atg caa tta aca aag ctt gga cac ggc tta	1104
Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu	
355 360 365	
cta tct ggg aag tac tca atg cct gca act cag aag gat gct aca act	1152
Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr	
370 375 380	
gga gat cct aga caa gaa gga ata cct cct cgc atg ttc aaa aac gta	1200
Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val	
385 390 395 400	
att gcc gcg agc cac gca gaa ttc tct tct atg aga cag cag gat gct	1248
Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala	
405 410 415	
ctc gac ttt ttc ctc cat ctg gta ggc aag gtt gag cgt gct agc aac	1296
Leu Asp Phe Phe Leu His Leu Val Gly Lys Val Glu Arg Ala Ser Asn	
420 425 430	
acg aca cca gat tta gac ccc tcg agg agc ttc aag ttt gga ata gaa	1344
Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu	
435 440 445	
gag aag atc ctt tgt ccg tct gga aag gtt gga tat aat aag agg gaa	1392
Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu	
450 455 460	
gac tgt att ctt tct ttg aac att ccg cta cat gag gca act aat aaa	1440
Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys	
465 470 475 480	
gat gaa tta gaa gcc ttt cac aag caa aaa gca gga aaa gga ttg gaa	1488
Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Leu Glu	
485 490 495	
gag aat gat atg agg tca agt gat gaa ata gta cgc cca cga gtt cct	1536
Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro	
500 505 510	
tta gaa gcc tgt cta gca aat ttt gca tca tca gag ccg att gaa gac	1584
Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp	
515 520 525	
tac tat agc tct gct ttg aag gga atg aca aca gct atc aag aca act	1632
Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr	
530 535 540	
ggt ttg aca tct ttc cca gat tat ttg gtc ttg cac atg cgg aaa ttt	1680
Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe	
545 550 555 560	
ggt atg gag gaa gcc tgg gtg cca aag aaa ctt gat gta tac att gat	1728
Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp	
565 570 575	
ggt ccg gat gtt att gat atc agc cac atg cgt agc aaa gga ctc caa	1776

Val Pro Asp Val Ile Asp Ile Ser His Met Arg Ser Lys Gly Leu Gln  
580 585 590

cct ggg gaa gaa ctg ttg cca gat ggc gtt cca gaa gaa gtg atg gaa 1824  
Pro Gly Glu Glu Leu Leu Pro Asp Gly Val Pro Glu Glu Val Met Glu  
595 600 605

tca gcg cag ccc gtg gca aat gag gag ata gtt gca cag cta gtc tca 1872  
Ser Ala Gln Pro Val Ala Asn Glu Glu Ile Val Ala Gln Leu Val Ser  
610 615 620

atg gga ttt agc cag ctt cac tgc cag aaa gct gcc ata aat act tcc 1920  
Met Gly Phe Ser Gln Leu His Cys Gln Lys Ala Ala Ile Asn Thr Ser  
625 630 635 640

aat gct ggg gtt gaa gag gca atg aac tgg tta ctt tct cac atg gat 1968  
Asn Ala Gly Val Glu Glu Ala Met Asn Trp Leu Leu Ser His Met Asp  
645 650 655

gat cca gac atc gat gca cca atc tcc cac cag aca tct gac att gat 2016  
Asp Pro Asp Ile Asp Ala Pro Ile Ser His Gln Thr Ser Asp Ile Asp  
660 665 670

caa tca agc gtt gat acc tta ctc tcc ttt ggt ttt gct gaa gat gtt 2064  
Gln Ser Ser Val Asp Thr Leu Leu Ser Phe Gly Phe Ala Glu Asp Val  
675 680 685

gct cgg aag gca cta aaa gcc tcg gga gga gac att gag aaa gca aca 2112  
Ala Arg Lys Ala Leu Lys Ala Ser Gly Gly Asp Ile Glu Lys Ala Thr  
690 695 700

gac tgg gta ttc aac aac cct aat gca tct gtt tca gac atg gat gta 2160  
Asp Trp Val Phe Asn Asn Pro Asn Ala Ser Val Ser Asp Met Asp Val  
705 710 715 720

tcc tct agc aat tca gcg cag act ccg gct caa agt gga tta cca gat 2208  
Ser Ser Ser Asn Ser Ala Gln Thr Pro Ala Gln Ser Gly Leu Pro Asp  
725 730 735

gga gga ggg aaa tac aag ctg ttt gga ata gta agt cac atg gga aca 2256  
Gly Gly Gly Lys Tyr Lys Leu Phe Gly Ile Val Ser His Met Gly Thr  
740 745 750

tca gtg cac tgt ggt cat tac gtg gct cac ata ttg aaa gaa ggc cgc 2304  
Ser Val His Cys Gly His Tyr Val Ala His Ile Leu Lys Glu Gly Arg  
755 760 765

tgg gta att ttc aat gac gac aaa gtt ggt atc tcg act gat cct cct 2352  
Trp Val Ile Phe Asn Asp Asp Lys Val Gly Ile Ser Thr Asp Pro Pro  
770 775 780

aaa gac atg ggt tat gtc tac ttc ttt cag cgg ctt gat tga 2394  
Lys Asp Met Gly Tyr Val Tyr Phe Phe Gln Arg Leu Asp  
785 790 795

&lt;210&gt; 30

&lt;211&gt; 797



&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 30

Met Glu Leu Leu Arg Ser Asn Leu Ser Arg Val Gln Ile Pro Glu Pro  
 1 5 10 15

Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro  
 20 25 30

Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe  
 35 40 45

Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val  
 50 55 60

Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro  
 65 70 75 80

Leu Lys Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Gly Phe Asp  
 85 90 95

Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro  
 100 105 110

Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val  
 115 120 125

Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys  
 130 135 140

Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His  
 145 150 155 160

Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser  
 165 170 175

Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn  
 180 185 190

Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr  
 195 200 205

Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro  
 210 215 220

Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp  
 225 230 235 240

Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala  
 245 250 255

Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr  
 260 265 270

Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp  
 275 280 285

Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly  
 290 295 300

Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala  
 305 310 315 320

Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr  
 325 330 335

Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp  
 340 345 350

Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu  
 355 360 365

Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr  
 370 375 380

Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val  
 385 390 395 400

Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala  
 405 410 415

Leu Asp Phe Phe Leu His Leu Val Gly Lys Val Glu Arg Ala Ser Asn  
 420 425 430

Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu  
 435 440 445

Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu  
 450 455 460

Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys  
 465 470 475 480

Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Leu Glu  
 485 490 495

Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro  
 500 505 510

Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp  
 515 520 525

Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr  
 530 535 540

Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe  
 545 550 555 560

Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp  
 565 570 575

Val Pro Asp Val Ile Asp Ile Ser His Met Arg Ser Lys Gly Leu Gln  
 580 585 590

Pro Gly Glu Glu Leu Leu Pro Asp Gly Val Pro Glu Glu Val Met Glu  
 595 600 605

Ser Ala Gln Pro Val Ala Asn Glu Glu Ile Val Ala Gln Leu Val Ser  
 610 615 620

Met Gly Phe Ser Gln Leu His Cys Gln Lys Ala Ala Ile Asn Thr Ser  
 625 630 635 640

Asn Ala Gly Val Glu Glu Ala Met Asn Trp Leu Leu Ser His Met Asp  
 645 650 655

Asp Pro Asp Ile Asp Ala Pro Ile Ser His Gln Thr Ser Asp Ile Asp  
 660 665 670

Gln Ser Ser Val Asp Thr Leu Leu Ser Phe Gly Phe Ala Glu Asp Val  
 675 680 685

Ala Arg Lys Ala Leu Lys Ala Ser Gly Gly Asp Ile Glu Lys Ala Thr  
690 695 700

Asp Trp Val Phe Asn Asn Pro Asn Ala Ser Val Ser Asp Met Asp Val  
705 710 715 720

Ser Ser Ser Asn Ser Ala Gln Thr Pro Ala Gln Ser Gly Leu Pro Asp  
725 730 735

Gly Gly Gly Lys Tyr Lys Leu Phe Gly Ile Val Ser His Met Gly Thr  
740 745 750

Ser Val His Cys Gly His Tyr Val Ala His Ile Leu Lys Glu Gly Arg  
755 760 765

Trp Val Ile Phe Asn Asp Asp Lys Val Gly Ile Ser Thr Asp Pro Pro  
770 775 780

Lys Asp Met Gly Tyr Val Tyr Phe Phe Gln Arg Leu Asp  
785 790 795

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<211> 1068

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1068)

<223> 15377

<400> 31

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tct ata gct cca tca ccg aag aag aag cct ctc atc ttc tta ggc tct 96  
Ser Ile Ala Pro Ser Pro Lys Lys Lys Pro Leu Ile Phe Leu Gly Ser  
20 25 30

cct cag gtc tcc gtg agt gtg ctt gaa gct ctt ttc aat gca tct aat 144  
Pro Gln Val Ser Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn  
35 40 45

gct cca aac tct tcc ttc gag gtt gca ggt att gtt aca cag cct cca Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro 50 55 60	192
tca agg aga gat agg ggt aaa aaa gtg ttg cct tca cca gta gcg caa Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln 65 70 75 80	240
tac gct ctt gat aaa ggc tta cct tct gat ctc att ttc tcc cct gag Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu 85 90 95	288
aag gca gga gat gaa gca ttt tta tgc gct tta aga gag ttg caa cct Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro 100 105 110	336
gag ctt tgt att aca gca gct tat ggg aat att ttg cct act aag ttc Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe 115 120 125	384
ctt aag att ccg gta cat ggg aca gtg aac ata cac cca agt ttg ctg Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu 130 135 140	432
ccg ctg tac cgt ggt gca gct cca gtt caa aga gca tta cag gat ggt Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly 145 150 155 160	480
gtc ccg gaa aca gga gta tca tta gca ttt act gtg cgt aag tta gat Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp 165 170 175	528
gca ggg cca gtg att gcc tct aag agg ttc caa gtg gat gat cta ata Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile 180 185 190	576
aag gca cca gaa cta ctc tgc ttc cta ttt tct gaa ggt tct aat ctt Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu 195 200 205	624
ctt atc cgt gaa ctt ccc tgc ata ttt gat ggg tcc gca aaa tca aaa Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys 210 215 220	672
gca gct ccc caa gat gat tct aaa gct acc tta gct cca aag ata gct Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala 225 230 235 240	720
cca gat gag gct tgg ctc tct ttt gac cag gaa gct ttt gtt cta cat Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His 245 250 255	768
aac aag gtt cgt gca ttt gca gga tgg ccg gga aca cga gca aaa gtt Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val 260 265 270	816
gta gtc ctt gat gag aaa agc ggt cag caa aat gtg cta gag ctt aaa Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys 275 280 285	864

att atg tcc act cga gta tgc aaa gat ctg gaa att cag gat agt gaa 912  
 ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu ile Gln Asp Ser Glu  
 290 295 300

caa gat tat gta act ttc aag aaa ggt tca cta ata ttt ccc tgc aga 960  
 Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu ile Phe Pro Cys Arg  
 305 310 315 320

gga ggt aca gct tta gag gta ctg gaa gtc cag ctt cct ggt aag aaa 1008  
 Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys  
 325 330 335

gcc atc aac gca gct gct ttt tgg aat ggc ttg aga ggt caa aag ctg 1056  
 Ala ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu  
 340 345 350

aag aag cta tga 1068  
 Lys Lys Leu  
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&lt;210&gt; 32

&lt;211&gt; 355

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 32

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Ser ile Ala Pro Ser Pro Lys Lys Lys Pro Leu ile Phe Leu Gly Ser  
 20 25 30

Pro Gln Val Ser Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn  
 35 40 45

Ala Pro Asn Ser Ser Phe Glu Val Ala Gly ile Val Thr Gln Pro Pro  
 50 55 60

Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln  
 65 70 75 80

Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu ile Phe Ser Pro Glu  
 85 90 95

Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro  
 100 105 110

Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe  
 115 120 125

Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu  
 130 135 140

Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly  
 145 150 155 160

Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp  
 165 170 175

Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile  
 180 185 190

Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu  
 195 200 205

Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys  
 210 215 220

Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala  
 225 230 235 240

Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His  
 245 250 255

Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val  
 260 265 270

Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys  
 275 280 285

Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu  
 290 295 300

Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu Ile Phe Pro Cys Arg  
 305 310 315 320

Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys  
 325 330 335

Ala Ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu  
 340 345 350

Lys Lys Leu  
355

<210> 33

<211> 2220

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2220)

<223> 16219

<400> 33

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aat cct ctc tcc tac tta gtc tcc att gat ggt ttc aac ttc ctc atc	96
Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile	
20 25 30	
gac tgt ggt tgg aac gat ctc ttc gac aca tcg ctc ctc gaa cct ctc	144
Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu	
35 40 45	
ccc agg gtt gct tct act ata gat gca gtt ttg ctt tct cat cca gat	192
Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp	
50 55 60	
aca ctt cac att ggt gct ctt cct tat gct atg aag cag ctt gga ctc	240
Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu	
65 70 75 80	
tcc gct cct gtt tat gct act gag cct gtt cat aga tta ggt ctc ctt	288
Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu	
85 90 95	
aca atg tat gat cag ttt ttg tcc agg aag caa gta tcc gac ttt gat	336
Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp	
100 105 110	
ctg ttt aca ctg gat gac ata gat tct gct ttc cag aat gtg atc aga	384
Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg	
115 120 125	
ttg act tac tct caa aat tac cat ctt tct gga aag gga gag ggt att	432



Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile	
130 135 140	
gta att gct cct cat gtt gct gga cac atg ctg gga ggt agc atc tgg	480
Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp	
145 150 155 160	
agg ata aca aag gat ggg gag gat gtt ata tat gct gtt gac tac aat	528
Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn	
165 170 175	
cat cgg aaa gaa agg cat ttg aat gga act gtt tta cag tct ttt gtt	576
His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val	
180 185 190	
cgg cct gct gtt ctg ata acc gat gca tat cat gct ctt tat acc aat	624
Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn	
195 200 205	
caa acc gca aga cag caa agg gac aaa gaa ttt cta gat acc att tca	672
Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser	
210 215 220	
aaa cat ctt gaa gtt gga gga aat gtt cta ttg cca gta gac act gcg	720
Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala	
225 230 235 240	
ggt cgt gtc ctg gaa ctt ctc ttg ata ctt gaa cag cat tgg tca caa	768
Gly Arg Val Leu Glu Leu Leu Leu Ile Leu Glu Gln His Trp Ser Gln	
245 250 255	
aga ggt ttc agc ttt ccc att tat ttt ctc acg tac gtg tca tct agc	816
Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser	
260 265 270	
aca att gac tat gtt aag agt ttc ctc gag tgg atg agt gac tcc att	864
Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile	
275 280 285	
tca aag tcc ttt gag act tca cgt gat aat gcc ttt cta ttg agg cat	912
Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His	
290 295 300	
gtc act ctg ttg ata aac aag act gat ctg gat aat gct cca cct ggt	960
Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly	
305 310 315 320	
cca aag gtt gtt ctt gct tcc atg gct agt ctc gaa gcc ggt ttt gct	1008
Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala	
325 330 335	
cga gag ata ttc gtg gag tgg gca aat gat ccc aga aat tta gtc ctc	1056
Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu	
340 345 350	
ttt act gaa aca ggc cag ttt ggc act tta gct cgt atg ctt cag tca	1104
Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser	
355 360 365	
gcc cca cct cca aaa ttt gtt aaa gtc acc atg tct aag agg gtt cct	1152

Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro	
370 375 380	
ttg gct ggg gaa gag tta att gca tat gag gaa gag caa aac aga ctg	1200
Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Glu Gln Asn Arg Leu	
385 390 395 400	
aaa agg gaa gaa gct ttg cga gct agc ctc gtt aaa gag gag gaa aca	1248
Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Glu Thr	
405 410 415	
aaa gct tcc cat gga tcc gat gat aat tca agt gaa cct atg atc ata	1296
Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile	
420 425 430	
gat acc aag act act cac gat gtt gtt ggt tct cac ggg cct gca tat	1344
Asp Thr Lys Thr Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr	
435 440 445	
aaa gat ata ttg att gat gga ttt gtt ccc cca tcg agc agc gta gct	1392
Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Ser Val Ala	
450 455 460	
cca atg ttc cca tat tat gat aac aca tct gaa tgg gac gac ttt ggg	1440
Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly	
465 470 475 480	
gag att att aat cca gat gac tat gtg atc aag gat gaa gac atg gac	1488
Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp	
485 490 495	
cga gga gca atg cat aac gga ggt gat gtg gac gga agg ctt gat gag	1536
Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu	
500 505 510	
gca act gct agt ctc atg ctt gat aca aga cct tcg aaa gtc atg tcc	1584
Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser	
515 520 525	
aat gag ctc att gtg act gtt agt tgt tca ctt gtt aaa atg gac tat	1632
Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr	
530 535 540	
gaa ggt cgg tca gat ggc cgc tca atc aag tca atg att gcg cat gtt	1680
Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val	
545 550 555 560	
tct cct cta aaa ctt gtt ttg gtg cac gcg ata gct gag gct aca gag	1728
Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu	
565 570 575	
cat ttg aag caa cac tgc ttg aac aac atc tgt cca cac gtg tat gct	1776
His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala	
580 585 590	
cct caa ata gag gaa acg gtc gat gtg act tct gat tta tgt gct tac	1824
Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr	
595 600 605	
aag gtc caa ctt tct gaa aag ctg atg agc aat gtg atc ttc aag aag	1872

Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys  
 610 615 620  
 ctg gga gat tca gaa gta gct tgg gtg gat tcc gaa gta ggg aag aca 1920  
 Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr  
 625 630 635 640  
 gag agg gac atg agg tct cta cta ccg atg cca ggt gct gct tcg cca 1968  
 Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro  
 645 650 655  
 cac aaa cct gtt cta gta ggt gat ctg aaa atc gca gac ttc aag cag 2016  
 His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln  
 660 665 670  
 ttt ctg tcg agc aag ggt gtt cag gta gaa ttt gca ggt gga gga gct 2064  
 Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Gly Ala  
 675 680 685  
 tta cgt tgt ggt gaa tat gtc act cta cga aag gtt gga ccg acg ggt 2112  
 Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly  
 690 695 700  
 caa aag gga gga gca tcg ggt cca cag caa att ctg ata gaa gga ccg 2160  
 Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro  
 705 710 715 720  
 ttg tgt gaa gac tat tac aaa atc agg gat tat ctc tat tct cag ttc 2208  
 Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe  
 725 730 735  
 tac ctc ctc tga 2220  
 Tyr Leu Leu

&lt;210&gt; 34

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 34

Met Gly Thr Ser Val Gln Val Thr Pro Leu Cys Gly Val Tyr Asn Glu  
 1 5 10 15

Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile  
 20 25 30

Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu  
 35 40 45

Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp  
 50 55 60

Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu  
 65 70 75 80

Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu  
 85 90 95

Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp  
 100 105 110

Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg  
 115 120 125

Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile  
 130 135 140

Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp  
 145 150 155 160

Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn  
 165 170 175

His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val  
 180 185 190

Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn  
 195 200 205

Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser  
 210 215 220

Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala  
 225 230 235 240

Gly Arg Val Leu Glu Leu Leu Leu Ile Leu Glu Gln His Trp Ser Gln  
 245 250 255

Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser  
 260 265 270

Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile  
 275 280 285

Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His  
 290 295 300

Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly  
 305 310 315 320

Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala  
 325 330 335

Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu  
 340 345 350

Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser  
 355 360 365

Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro  
 370 375 380

Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Glu Gln Asn Arg Leu  
 385 390 395 400

Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Glu Thr  
 405 410 415

Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile  
 420 425 430

Asp Thr Lys Thr Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr  
 435 440 445

Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Ser Val Ala  
 450 455 460

Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly  
 465 470 475 480

Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp  
 485 490 495

Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu  
 500 505 510

Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser  
 515 520 525

Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr  
 530 535 540

Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val  
 545 550 555 560

Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu  
 565 570 575

His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala  
 580 585 590

Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr  
 595 600 605

Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys  
 610 615 620

Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr  
 625 630 635 640

Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro  
 645 650 655

His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln  
 660 665 670

Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Gly Ala  
 675 680 685

Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly  
 690 695 700

Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro  
 705 710 715 720

Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe  
 725 730 735

Tyr Leu Leu

<210> 35

<211> 1116

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1116)

&lt;223&gt;

&lt;400&gt; 35

atg gca gca gcg atg tct tct tct tgt tgc gct tcc tcg ctt cgt tta	48
Met Ala Ala Ala Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu	
1 5 10 15	
atc cca ttc aaa cgg acc ttg ttt tct tca atc cat tat ccg gcc aaa	96
Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys	
20 25 30	
acc ctt ctt cta cga cca cta aaa ccg tcg gaa gtt cct tcc ttt cgc	144
Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg	
35 40 45	
cgg acg atc atc act ttc cag aaa att tca acc ggg att gtt cct cca	192
Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro	
50 55 60	
cca tcg gct tca tca tct ccg tcg agc tat gga gac ctt caa cca atc	240
Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile	
65 70 75 80	
gaa gag ctt cca ccg aag cta caa gag atc gtc aag ctt ttc caa tcg	288
Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser	
85 90 95	
gta caa gag cca aag gct aaa tac gag cag ctt atg ttc tac ggg aag	336
Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys	
100 105 110	
aat ctg aca cct ctc gat tct caa ttc aag acg agg gag aat aaa gta	384
Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val	
115 120 125	
gaa gga tgt gtt tct cag gtt tgg gtt agg gct ttc ttt gat gag gaa	432
Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu	
130 135 140	
cgt aat gtt gtg tat gaa gct gat tct gat tcg gtt ctc act aaa ggg	480
Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly	
145 150 155 160	
tta gct gct cta tta gtc aag ggt tta tct gga aga cct gtc cct gag	528
Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu	
165 170 175	

att ttg agg ata aca cct gat ttc gct gtt ctt ctc ggg ttg cag cag Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln 180 185 190	576
agt ctg tct cct tct aga aac aat gga tta ctt aat atg ctt aag ctg Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu 195 200 205	624
atg cag aaa aag gct ctt cat ttg gaa gtc aaa ggt gag gaa gat tca Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser 210 215 220	672
agt tct gga gag agt tca gaa tcc agc ttt gtg tct att cct gag act Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr 225 230 235 240	720
aag gac gaa gct aat gtt ccg gag gtg gat ttg gag tct aaa cct gat Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp 245 250 255	768
cta gtt gag gat ttg gga aca gaa aag att gat gat tct gag agt ggg Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly 260 265 270	816
tca aat gtt gtt gct tta ggg agt aga ggg atg agg ata aga gag aaa Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys 275 280 285	864
ttg gag aag gag cta gat cct gtt gag tta gaa gtt gaa gat gtt tct Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser 290 295 300	912
tac cag cac gca gga cat gcc gct gtt aga ggt agt gct ggt gat gat Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp 305 310 315 320	960
ggg gaa aca cat ttc aac ttg cga atc gtt tcg gat gct ttc caa ggt Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly 325 330 335	1008
aaa agc ttg gtc aag aga cat agg ctg ata tat gac ttg ttg caa gat Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp 340 345 350	1056
gag ttg aag agc ggg tta cat gct ctc tct att gtg gca aag act cct Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro 355 360 365	1104
gct gag gtt tga Ala Glu Val 370	1116

&lt;210&gt; 36

&lt;211&gt; 371

&lt;212&gt; PRT



&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 36

Met Ala Ala Ala Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu  
 1 5 10 15

Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys  
 20 25 30

Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg  
 35 40 45

Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro  
 50 55 60

Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile  
 65 70 75 80

Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser  
 85 90 95

Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys  
 100 105 110

Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val  
 115 120 125

Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu  
 130 135 140

Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly  
 145 150 155 160

Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu  
 165 170 175

Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln  
 180 185 190

Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu  
 195 200 205

Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser  
 210 215 220

Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr  
 225 230 235 240

Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp  
 245 250 255

Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly  
 260 265 270

Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys  
 275 280 285

Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser  
 290 295 300

Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp  
 305 310 315 320

Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly  
 325 330 335

Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp  
 340 345 350

Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro  
 355 360 365

Ala Glu Val  
 370

<210> 37

<211> 1059

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1059)

<223> 20933

&lt;400&gt; 37

atg gat ttg atg gag aag aac ttg gag tta gtg gag att cag aaa cta	48
Met Asp Leu Met Glu Lys Asn Leu Glu Leu Val Glu Ile Gln Lys Leu	
1 5 10 15	
 gaa ggc cac acc gat cgt gtt tgg agc gta gct tgg aac ccc gtt tct	96
Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser	
20 25 30	
 tct cac gcc gac ggt gtt tca ccg att ctt gct tct tgc agt ggc gat	144
Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp	
35 40 45	
 aac act gtt cga atc tgg gaa caa agc tct ctc tct cgc tcc tgg act	192
Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr	
50 55 60	
 tgc aag aca gtt ttg gaa gag acg cat aca aga act gtg agg tcg tgc	240
Cys Lys Thr Val Leu Glu Glu Thr His Thr Arg Thr Val Arg Ser Cys	
65 70 75 80	
 gct tgg tca ccc tca gga cag tta ttg gcc act gca agt ttt gat ggt	288
Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly	
85 90 95	
 acc act ggc att tgg aag aat tac ggt tct gag ttt gag tgt att tcc	336
Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser	
100 105 110	
 act ttg gag gga cat gaa aac gaa gtc aaa agt gta tca tgg aat gca	384
Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala	
115 120 125	
 tct ggt tca tgc ctt gca aca tgt agt aga gat aag tct gtt tgg att	432
Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile	
130 135 140	
 tgg gaa gtg ctt gaa ggg aat gaa tat gac tgt gct gcg gta tta act	480
Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr	
145 150 155 160	
 ggg cat aca caa gat gtg aag atg gtt cag tgg cat ccc acc atg gat	528
Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp	
165 170 175	
 gtt tta ttt tct tgc agt tat gat aac acc atc aag gtt tgg tgg tct	576
Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser	
180 185 190	
 gaa gat gat gat ggt gag tat caa tgt gtc caa acc tta ggt gaa tct	624
Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser	
195 200 205	
 aac aac ggt cac tct tca acg gta tgg tcc atc tca ttt aac gct gca	672
Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala	
210 215 220	
 ggg gac aag atg gtc act tgt agt gat gat cta acc ttg aag ata tgg	720

Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp  
 225 230 235 240  
 ggg aca gat att gcc aag atg cag tct ggt gaa gaa tat gca cct tgg 768  
 Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp  
 245 250 255  
 att cat ctt tgt act ctc tct ggc tat cat gac cgt acc ata tac tca 816  
 Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser  
 260 265 270  
 gct cac tgg tca agg gac gac att att gcc agt gga gca ggc gat aat 864  
 Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn  
 275 280 285  
 gct ata cgg ttg ttt gtg gac agc aaa cat gac tct gtt gat gga cct 912  
 Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro  
 290 295 300  
 tca tat aat ctt ttg ctg aag aag aat aaa gca cat gaa aat gat gta 960  
 Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val  
 305 310 315 320  
 aac tct gtc caa tgg tca ccc ggt gag ggg aac cgg ttg ctt gcg tcg 1008  
 Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser  
 325 330 335  
 gct agt gat gat ggg atg gtc aag att tgg cag ctt gca act aaa ccg 1056  
 Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro  
 340 345 350  
 tga 1059

&lt;210&gt; 38

&lt;211&gt; 352

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 38

Met Asp Leu Met Glu Lys Asn Leu Glu Leu Val Glu Ile Gln Lys Leu  
 1 5 10 15

Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser  
 20 25 30

Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp  
 35 40 45

Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr  
 50 55 60

Cys Lys Thr Val Leu Glu Glu Thr His Thr Arg Thr Val Arg Ser Cys  
 65 70 75 80

Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly  
 85 90 95

Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser  
 100 105 110

Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala  
 115 120 125

Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile  
 130 135 140

Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr  
 145 150 155 160

Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp  
 165 170 175

Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser  
 180 185 190

Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser  
 195 200 205

Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala  
 210 215 220

Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp  
 225 230 235 240

Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp  
 245 250 255

Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser  
 260 265 270

Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn  
 275 280 285

Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro  
 290 295 300

Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val  
 305 310 315 320

Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser  
 325 330 335

Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro  
 340 345 350

<210> 39

<211> 942

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (924)

<223>

<400> 39  
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 Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg  
 1 5 10 15  
 gaa tca tca act aag ctc ttc acc aaa aag cct aac aat gtt gtg gtt 96  
 Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val  
 20 25 30  
 tgt gcg gcg aga ggt cca aga cct cgg tct cct cgt gta tgg aaa aca 144  
 Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr  
 35 40 45  
 agg aag agg att gga act atc tct aaa gct gcc aaa atg att gct tgt 192  
 Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys  
 50 55 60  
 ata aaa gga ttg tcg aat gtt aaa gaa gaa gtt tat gga gcg ctt gat 240  
 Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp  
 65 70 75 80  
 tcc ttc att gct tgg gaa tta gag ttc cct ctt gtt ata gtt aag aag 288  
 Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys  
 85 90 95  
 gca tta gtt ata ctt gaa gat gaa aaa gaa tgg aag aag att att cag 336  
 Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln

100	105	110	
gtg aca aaa tgg atg ctg agt	aaa ggc caa gga aga	aca atg gga act	384
Val Thr Lys Trp Met Leu Ser	Lys Gly Gln Gly Arg	Thr Met Gly Thr	
115	120	125	
tac ttc tca tta cta aat gct	tta gca gaa gat aat	cgc ctt gac gaa	432
Tyr Phe Ser Leu Leu Asn Ala	Leu Ala Glu Asp Asn	Arg Leu Asp Glu	
130	135	140	
gct gag gaa ttg tgg aac aaa	ttg ttc atg gaa cat tta	gaa gga act	480
Ala Glu Glu Leu Trp Asn Lys	Leu Phe Met Glu His	Leu Glu Gly Thr	
145	150	155	160
cct aga aag ttc ttc aac aaa	atg atc tct ata tat tac	aag aga gat	528
Pro Arg Lys Phe Phe Asn Lys	Met Ile Ser Ile Tyr Tyr	Lys Arg Asp	
165	170	175	
atg cac caa aag ctc ttc gag	gtc ttt gct gac atg gag	gag ctt gga	576
Met His Gln Lys Leu Phe Glu	Val Phe Ala Asp Met	Glu Glu Leu Gly	
180	185	190	
gtg aaa ccg aat gtt gcg att	gtg tct atg gtt gga aaa	gtg ttt gtg	624
Val Lys Pro Asn Val Ala Ile	Val Ser Met Val Gly Lys	Val Phe Val	
195	200	205	
aaa cta gag atg aag gat aag	tac gag aaa ctg atg aag	aaa tat cct	672
Lys Leu Glu Met Lys Asp Lys	Tyr Glu Lys Leu Met Lys	Lys Lys Tyr Pro	
210	215	220	
cca cca cag tgg gag ttt aga	tac atc aaa gga aga cgt	gtt aag gtc	720
Pro Pro Gln Trp Glu Phe Arg	Tyr Ile Lys Gly Arg Arg	Val Lys Val	
225	230	235	240
aag gca aag cag ctg aat gag	cta agc gaa ggt gaa ggt	ggt tta agc	768
Lys Ala Lys Gln Leu Asn Glu	Leu Ser Glu Gly Glu Gly	Gly Leu Ser	
245	250	255	
agc gac gaa gat aag att gac	aat gag att gag agt gaa	gaa gaa gat	816
Ser Asp Glu Asp Lys Ile Asp	Asn Glu Ile Glu Ser Glu	Glu Glu Asp	
260	265	270	
ggt gag gat ctc agt gaa gag	gaa gaa gat gaa aaa gaa	ctt ttg ggt	864
Gly Glu Asp Leu Ser Glu Glu	Glu Glu Asp Glu Lys Glu	Leu Leu Gly	
275	280	285	
gga agt caa gga cag att act	tct aga gaa ccc agt ctt	gat cat ttg	912
Gly Ser Gln Gly Gln Ile Thr	Ser Arg Glu Pro Ser Leu	Asp His Leu	
290	295	300	
gac tct tca tga			924
Asp Ser Ser			
305			

&lt;210&gt; 40

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 40

Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg  
 1 5 10 15

Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val  
 20 25 30

Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr  
 35 40 45

Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys  
 50 55 60

Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp  
 65 70 75 80

Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys  
 85 90 95

Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln  
 100 105 110

Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr  
 115 120 125

Tyr Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu  
 130 135 140

Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr  
 145 150 155 160

Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp  
 165 170 175

Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly  
 180 185 190

Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val  
 195 200 205



Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro  
 210 215 220

Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val  
 225 230 235 240

Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Gly Leu Ser  
 245 250 255

Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Glu Asp  
 260 265 270

Gly Glu Asp Leu Ser Glu Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly  
 275 280 285

Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu  
 290 295 300

Asp Ser Ser  
 305

<210> 41

<211> 2427

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2427)

<223> 21878

<400> 41

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 Met Val Lys Glu Thr Leu Ile Pro Pro Ser Ser Thr Ser Met Thr Thr  
 1 5 10 15

48

gga aca tct tct tct tcg tct ctt tca atg acg tta tcc tca aca aac  
 Gly Thr Ser Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn  
 20 25 30

96

gcg tta tcg ttt ttg tcg aaa gga tgg aga gag gta tgg gat tca gca  
 Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala

144

35	40	45	
gat gcg gat ttg cag ctg atg cga gac aga gct aac tct gtt aag aat			192
Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn			
50	55	60	
cta gca tca acg ttc gat aga gag atc gag aat ttc ctc aat aac tcg			240
Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser			
65	70	75	80
gcg agg tct gcg ttt ccc gtt ggt tca cca tcg gcg tcg tct ttc tca			288
Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser			
	85	90	95
aat gaa att ggt atc atg aag aag ctt cag ccg aag att tcg gag ttt			336
Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe			
	100	105	110
cgt agg gtt tat tcg gcg ccg gag att agt cgc aag gtt atg gag aga			384
Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg			
	115	120	125
tgg gga cct gcg aga gcg aag ctt gga atg gat cta tcg gcg att aag			432
Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys			
	130	135	140
aag gcg att gtg tct gag atg gaa ttg gat gag cgt cag gga gtt ttg			480
Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu			
	145	150	155
gag atg agt aga ttg agg aga cgg cgt aat agt gat agg gtt agg ttt			528
Glu Met Ser Arg Leu Arg Arg Arg Arg Asn Ser Asp Arg Val Arg Phe			
	165	170	175
acg gag ttt ttc gcg gag gct gag aga gat gga gaa gct tat ttc ggt			576
Thr Glu Phe Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly			
	180	185	190
gat tgg gaa ccg att agg tct ttg aag agt aga ttt aaa gag ttt gag			624
Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu			
	195	200	205
aaa cga agc tcg tta gaa ata ttg agt gga ttc aag aac agt gaa ttt			672
Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe			
	210	215	220
gtt gag aag ctc aaa acc agc ttt aaa tca att tac aaa gaa act gat			720
Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp			
	225	230	235
gag gct aag gat gtc cct ccg ttg gat gta cct gaa ctg ttg gca tgt			768
Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys			
	245	250	255
ttg gtt aga caa tct gaa cct ttt ctt gat cag att ggt gtt aga aag			816
Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys			
	260	265	270
gat aca tgt gac cga ata gta gaa agc ctt tgc aaa tgc aag agc caa			864
Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln			

275	280	285	
caa ctt tgg cgt ctg cca tct gca caa gca tcc gat tta att gaa aat			912
Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn			
290	295	300	
gat aac cat gga gtt gat ttg gat atg agg ata gcc agt gtt ctt caa			960
Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln			
305	310	315	320
agc aca gga cac cat tat gat ggt ggg ttt tgg act gat ttt gtg aag			1008
Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys			
	325	330	335
cct gag aca ccg gaa aac aaa agg cat gtg gca att gtt aca aca gct			1056
Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala			
	340	345	350
agt ctt cct tgg atg acc gga aca gct gta aat ccg cta ttc aga gcg			1104
Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala			
	355	360	365
gcg tat ttg gca aaa gct gca aaa cag agt gtt act ctc gtg gtt cct			1152
Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro			
	370	375	380
tgg ctc tgc gaa tct gat caa gaa cta gtg tat cca aac aat ctc acc			1200
Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr			
385	390	395	400
ttc agc tca cct gaa gaa caa gag agt tat ata cgt aaa tgg ttg gag			1248
Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu			
	405	410	415
gaa agg att ggt ttc aag gct gat ttt aaa atc tcc ttt tac cca gga			1296
Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly			
	420	425	430
aag ttt tca aaa gaa agg cgc agc ata ttt cct gct ggt gac act tct			1344
Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser			
	435	440	445
caa ttt ata tcg tca aaa gat gct gac att gct ata ctt gaa gaa cct			1392
Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro			
	450	455	460
gaa cat ctc aac tgg tat tat cac ggc aag cgt tgg act gat aaa ttc			1440
Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe			
465	470	475	480
aac cat gtt gtt gga att gtc cac aca aac tac tta gag tac atc aag			1488
Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys			
	485	490	495
agg gag aag aat gga gct ctt caa gca ttt ttt gtg aac cat gta aac			1536
Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn			
	500	505	510
aat tgg gtc aca cga gcg tat tgt gac aag gtt ctt cgc ctc tct gcg			1584
Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala			

515	520	525	
gca aca caa gat tta cca aag tct gtt gta tgc aat gtc cat ggt gtc			1632
Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val			
530	535	540	
aat ccc aag ttc ctt atg att ggg gag aaa att gct gaa gag aga tcc			1680
Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser			
545	550	555	560
cgt ggt gaa caa gct ttc tca aaa ggt gca tac ttc tta gga aaa atg			1728
Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met			
565	570	575	
gtg tgg gct aaa gga tac aga gaa cta ata gat ctg atg gct aaa cac			1776
Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His			
580	585	590	
aaa agc gaa ctt ggg agc ttc aat cta gat gta tat ggg aac ggt gaa			1824
Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu			
595	600	605	
gat gca gtc gag gtc caa cgt gca gca aag aaa cat gac ttg aat ctc			1872
Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu			
610	615	620	
aat ttc ctc aaa gga agg gac cac gct gac gat gct ctt cac aag tac			1920
Asn Phe Leu Lys Gly Arg Asp His Ala Asp Asp Ala Leu His Lys Tyr			
625	630	635	640
aaa gtg ttc ata aac ccc agc atc agc gat gtt cta tgc aca gca acc			1968
Lys Val Phe Ile Asn Pro Ser Ile Ser Asp Val Leu Cys Thr Ala Thr			
645	650	655	
gca gaa gca cta gcc atg ggg aag ttt gtg gtg tgt gca gat cac cct			2016
Ala Glu Ala Leu Ala Met Gly Lys Phe Val Val Cys Ala Asp His Pro			
660	665	670	
tca aac gaa ttc ttt aga tca ttc ccg aac tgc tta act tac aaa aca			2064
Ser Asn Glu Phe Phe Arg Ser Phe Pro Asn Cys Leu Thr Tyr Lys Thr			
675	680	685	
tcc gaa gac ttt gtg tcc aaa gtg caa gaa gca atg acg aaa gag cca			2112
Ser Glu Asp Phe Val Ser Lys Val Gln Glu Ala Met Thr Lys Glu Pro			
690	695	700	
cta cct ctc act cct gaa caa atg tac aat ctc tct tgg gaa gca gca			2160
Leu Pro Leu Thr Pro Glu Gln Met Tyr Asn Leu Ser Trp Glu Ala Ala			
705	710	715	720
aca cag agg ttc atg gag tat tca gat ctc gat aag atc tta aac aat			2208
Thr Gln Arg Phe Met Glu Tyr Ser Asp Leu Asp Lys Ile Leu Asn Asn			
725	730	735	
gga gag gga gga agg aag atg cga aaa tca aga tcg gtt ccg agc ttt			2256
Gly Glu Gly Gly Arg Lys Met Arg Lys Ser Arg Ser Val Pro Ser Phe			
740	745	750	
aac gag gtg gtc gat gga gga ttg gca ttc tca cac tat gtt cta aca			2304
Asn Glu Val Val Asp Gly Gly Leu Ala Phe Ser His Tyr Val Leu Thr			

755                      760                      765  
 ggg aac gat ttc ttg aga cta tgc act gga gca aca cca aga aca aaa      2352  
 Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys  
 770                      775                      780  
 gac tat gat aat caa cat tgc aag gat ctg aat ctc gta cca cct cac      2400  
 Asn Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His  
 785                      790                      795                      800  
 gtt cac aag cca atc ttc ggc tgg tag      2427  
 Val His Lys Pro Ile Phe Gly Trp  
 805

&lt;210&gt; 42

&lt;211&gt; 808

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 42

Met Val Lys Glu Thr Leu Ile Pro Pro Ser Ser Thr Ser Met Thr Thr  
 1                      5                      10                      15  
 Gly Thr Ser Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn  
 20                      25                      30  
 Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala  
 35                      40                      45  
 Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn  
 50                      55                      60  
 Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser  
 65                      70                      75                      80  
 Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser  
 85                      90                      95  
 Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe  
 100                      105                      110  
 Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg  
 115                      120                      125  
 Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys

130                                      135                                      140  
 Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu  
 145                                      150                                      155                                      160  
 Glu Met Ser Arg Leu Arg Arg Arg Arg Asn Ser Asp Arg Val Arg Phe  
 165                                      170                                      175  
 Thr Glu Phe Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly  
 180                                      185                                      190  
 Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu  
 195                                      200                                      205  
 Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe  
 210                                      215                                      220  
 Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp  
 225                                      230                                      235                                      240  
 Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys  
 245                                      250                                      255  
 Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys  
 260                                      265                                      270  
 Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln  
 275                                      280                                      285  
 Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn  
 290                                      295                                      300  
 Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln  
 305                                      310                                      315                                      320  
 Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys  
 325                                      330                                      335  
 Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala  
 340                                      345                                      350  
 Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala  
 355                                      360                                      365  
 Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro

370                      375                      380  
 Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr  
 385                      390                      395                      400  
 Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu  
                     405                      410                      415  
 Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly  
                     420                      425                      430  
 Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser  
                     435                      440                      445  
 Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro  
                     450                      455                      460  
 Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe  
 465                      470                      475                      480  
 Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys  
                     485                      490                      495  
 Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn  
                     500                      505                      510  
 Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala  
                     515                      520                      525  
 Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val  
                     530                      535                      540  
 Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser  
 545                      550                      555                      560  
 Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met  
                     565                      570                      575  
 Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His  
                     580                      585                      590  
 Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu  
                     595                      600                      605  
 Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu

610                                      615                                      620  
 Asn Phe Leu Lys Gly Arg Asp His Ala Asp Asp Ala Leu His Lys Tyr  
 625                                      630                                      635                                      640  
 Lys Val Phe Ile Asn Pro Ser Ile Ser Asp Val Leu Cys Thr Ala Thr  
 645                                      650                                      655  
 Ala Glu Ala Leu Ala Met Gly Lys Phe Val Val Cys Ala Asp His Pro  
 660                                      665                                      670  
 Ser Asn Glu Phe Phe Arg Ser Phe Pro Asn Cys Leu Thr Tyr Lys Thr  
 675                                      680                                      685  
 Ser Glu Asp Phe Val Ser Lys Val Gln Glu Ala Met Thr Lys Glu Pro  
 690                                      695                                      700  
 Leu Pro Leu Thr Pro Glu Gln Met Tyr Asn Leu Ser Trp Glu Ala Ala  
 705                                      710                                      715                                      720  
 Thr Gln Arg Phe Met Glu Tyr Ser Asp Leu Asp Lys Ile Leu Asn Asn  
 725                                      730                                      735  
 Gly Glu Gly Gly Arg Lys Met Arg Lys Ser Arg Ser Val Pro Ser Phe  
 740                                      745                                      750  
 Asn Glu Val Val Asp Gly Gly Leu Ala Phe Ser His Tyr Val Leu Thr  
 755                                      760                                      765  
 Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys  
 770                                      775                                      780  
 Asp Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His  
 785                                      790                                      795                                      800  
 Val His Lys Pro Ile Phe Gly Trp  
 805

<210> 43

<211> 1299

<212> DNA

<213> Arabidopsis thaliana



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1299)

&lt;223&gt; 23915

&lt;400&gt; 43

atg gga gct agg gtt caa gta caa cat tac aat tta gga tca tct gat	48
Met Gly Ala Arg Val Gln Val Gln His Tyr Asn Leu Gly Ser Ser Asp	
1 5 10 15	
tcc tac atc gct act tct ctc cac gat ctc aac tcc gtc gat ggt ccg	96
Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro	
20 25 30	
ccg aga gat atc gac ggt atc gga ggc gcc gtt ggt cgt gac ggc gat	144
Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp	
35 40 45	
agt tta gat aat gac ggc gat tcc tct tct gcg gac tgt atg cat gaa	192
Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu	
50 55 60	
tca tac aga aac tct atg caa atc gga gta gaa gaa ggt gga tct aac	240
Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Gly Ser Asn	
65 70 75 80	
atg gag aac aaa gga tct gct tac att atg tta aac att gaa gat gtt	288
Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val	
85 90 95	
tca ccg att gaa gca gca aga ggg agg ttt ctg caa atc ata ttg gac	336
Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp	
100 105 110	
tac ttt att agc caa cat gtg att gaa gtc tgt gag agc aaa cgt gat	384
Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp	
115 120 125	
cat gat gtg gat tca gga gga cgt gat agt aat agt aaa gtg aag agg	432
His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg	
130 135 140	
aag tcg gat gat acg cga tat gaa ggt gat ccg agt ttt gcg tta ccg	480
Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro	
145 150 155 160	
ttg atg tat att gca aat ttg tat gag act tta gtt ggt gaa gca aat	528
Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn	
165 170 175	
gtg agg ctt gct tca ttg aat gga ata agg gat aag act att gga gta	576
Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val	
180 185 190	

gct ctt gaa gct gct ggt ggc ttg tat agg aaa tta act aag aag ttt Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe 195 200 205	624
cct aag aaa ggt act tgc atg tac agg aga aga gaa ctg gca act tca Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser 210 215 220	672
gtt gaa aca agg aca aga ttt cca gaa ttg gta ata cat gaa gag aaa Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys 225 230 235 240	720
cga gtt cgc ttt gtg gtg gtt aat ggt ttg gat att gtt gaa aag cca Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro 245 250 255	768
agt gat ttg cct att gaa gaa gct gaa tgg ttt aag cga tta aca ggc Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly 260 265 270	816
cgt aat gaa gtg gct atc tct gct aga gat tat aaa ttc tac tgc cct Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro 275 280 285	864
cga cgc aag cat agg cgt ctt cag aat tct gtc tcc agc atc aat ggc Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly 290 295 300	912
ttg cct aca ttt cca ggt ata gac tct tca acg tta gct aat aca caa Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln 305 310 315 320	960
gga ttt cgc gaa gat caa agc caa caa caa cac act cct tct cct tcc Gly Phe Arg Glu Asp Gln Ser Gln Gln His Thr Pro Ser Pro Ser 325 330 335	1008
aaa cat cat atg tca tct ttg tct cat caa ttt cat caa tct att cac Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His 340 345 350	1056
cag agc cac caa cac cat caa tct ata tac caa agt caa cac gca gcc Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala 355 360 365	1104
aca cac tat ccc agt cag aac cat caa tgt gac cct gaa cta tct cac Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His 370 375 380	1152
aca caa atg gct tgc ttg caa ccc etc act gga ggc cat gta atg cca Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro 385 390 395 400	1200
aat agt ccg gcg aaa ttt tgt gac caa tgt gga gca cag tac ttg aga Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg 405 410 415	1248
gag aca tcc aaa ttc tgc tca gag tgt ggt tcc aag aga ctc ggg ata Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile 420 425 430	1296

tag

1299

&lt;210&gt; 44

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 44

Met Gly Ala Arg Val Gln Val Gln His Tyr Asn Leu Gly Ser Ser Asp  
 1 5 10 15

Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro  
 20 25 30

Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp  
 35 40 45

Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu  
 50 55 60

Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Gly Ser Asn  
 65 70 75 80

Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val  
 85 90 95

Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp  
 100 105 110

Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp  
 115 120 125

His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg  
 130 135 140

Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro  
 145 150 155 160

Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn  
 165 170 175

Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val  
 180 185 190

Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe  
 195 200 205

Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser  
 210 215 220

Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys  
 225 230 235 240

Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro  
 245 250 255

Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly  
 260 265 270

Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro  
 275 280 285

Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly  
 290 295 300

Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln  
 305 310 315 320

Gly Phe Arg Glu Asp Gln Ser Gln Gln Gln His Thr Pro Ser Pro Ser  
 325 330 335

Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His  
 340 345 350

Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala  
 355 360 365

Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His  
 370 375 380

Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro  
 385 390 395 400

Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg  
 405 410 415

Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile  
                   420                  425                  430

<210> 45

<211> 1617

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1617)

<223> 30945

<400> 45

atg aat gag gac aaa aat cct gct agg gct att gac ttg gct gcc agt 48  
 Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser  
 1                  5                  10                  15

aat agc atg tat tta cgt gag acc ata ctt tct agt gaa tct cct agt 96  
 Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser  
                   20                  25                  30

ctc aac act cag aat atc tca gtg aca gtt gaa atg cca ccc atg ttg 144  
 Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu  
                   35                  40                  45

aaa ccg ttg cat ggg cat ctt ctt aaa cac ttt att gtg ttt tca aat 192  
 Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn  
                   50                  55                  60

att gaa gac cag aac agt atc atc ata ata att cat gct act aac aat 240  
 Ile Glu Asp Gln Asn Ser Ile Ile Ile Ile Ile His Ala Thr Asn Asn  
 65                  70                  75                  80

tgt cta cag cgt tgc ccg tca gtt act aaa gaa cag tgg gca gtg cca 288  
 Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro  
                   85                  90                  95

gcg att ttg tct tct ttg aaa atg gaa gaa aac ctt ttg gcc cag gaa 336  
 Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu  
                   100                  105                  110

agg gcc tgt gtg ttc ctc tcc ttg ttg ctg cat aac ttc tcc atg gtt 384  
 Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val  
                   115                  120                  125

cac aca aca aaa act ggg aat act ctg aat gtt gat tct ttc tcc tgc 432  
 His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys  
                   130                  135                  140

ttg gat tct ttc tca aag cat ata cgt ggt ggt atg gct gat act gaa Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu 145 150 155 160	480
gct gga gtt atg ctt tct gga ttt tcg gaa gaa ctc ctt tgt ctt ctt Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu 165 170 175	528
cag gac ctc ctt tct ggg cag cgg gta tta ttt tcg gtt aaa tcc tca Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser 180 185 190	576
gaa aca tgt gaa tct gat tta agc atc cct gtc acc ctg aat gga gaa Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu 195 200 205	624
aat gta gct ctc gtc aac aaa atc gct cta act gat caa ttg gtg gcc Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala 210 215 220	672
gga agc gct att ttg gcg gca ata tgt act gca ctt gat cgt att gga Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly 225 230 235 240	720
tat atc tgc gaa gct tcc ttt gaa atc ctg cac aag tac agt cat gag Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu 245 250 255	768
aaa acc tca gtg cta ctg acc att ctt cac gtt ttt gct tac att gct Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala 260 265 270	816
gga gag aaa atg gtg ttg tct agt gag cat ggc ata tca att gca gtg Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val 275 280 285	864
ttg aaa tac att gtc atg ttt cta gaa aac aaa cat ttt ggt act gtg Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val 290 295 300	912
gag ggc agt tct cga ttg cac cca ggc aag aac aag tgt cca ttc tca Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser 305 310 315 320	960
gac agg tct tcc tcg ctg gag gct atg gca tct aag ctc atg gaa att Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile 325 330 335	1008
ctt cag gaa ttt act gag tct aat act ttg cat aaa agc ttg act ggt Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly 340 345 350	1056
tca ttg ggt tct agc cac cta gag aag acc gag ttt agg ccg gca cac Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His 355 360 365	1104
aaa gat ttc cag tgt gta ttg acc agg gat caa agt atc aat ctc tgt Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys 370 375 380	1152

gac att cta tca ttg gtg gag ctt att gct tgt tat acg gct tgg gat 1200  
 Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp  
 385 390 395 400

tgg act agt gcg aac att gtt gct cca ctg ctt aag atg ctg gga atg 1248  
 Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met  
 405 410 415

cca ttg cca atg aac ctc tct gtt gca atc gtc tcc ctt ctt ggg caa 1296  
 Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln  
 420 425 430

ctt agc agt att gga gtg gat gct ggt ggc tat gaa aac gaa gga atc 1344  
 Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile  
 435 440 445

tca aac ttg aga gtg aaa ctg tca gca ttt cta cag tgt gag acg aca 1392  
 Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr  
 450 455 460

cta aag gcc ggt ttt gca gtg cag ata gca act gtg agc tcc ctc ctg 1440  
 Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu  
 465 470 475 480

aag acg ctg cag ctg aaa ttc cca ata gac ttt caa gac aaa acc acc 1488  
 Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr  
 485 490 495

atg att ccg ggt agt ggc gac caa agc tta tct ggt tca gtc aat gtg 1536  
 Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val  
 500 505 510

gtg acc aag tgg ttg tcg ttg ttg agc aag gaa caa cga gtt ttc gca 1584  
 Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala  
 515 520 525

ttt gag ttt cta caa acc aat gtt gtt aga tga 1617  
 Phe Glu Phe Leu Gln Thr Asn Val Val Arg  
 530 535

&lt;210&gt; 46

&lt;211&gt; 538

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 46

Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser  
 1 5 10 15

Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser  
 20 25 30

Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu  
 35 40 45

Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn  
 50 55 60

Ile Glu Asp Gln Asn Ser Ile Ile Ile Ile Ile His Ala Thr Asn Asn  
 65 70 75 80

Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro  
 85 90 95

Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu  
 100 105 110

Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val  
 115 120 125

His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys  
 130 135 140

Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu  
 145 150 155 160

Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu  
 165 170 175

Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser  
 180 185 190

Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu  
 195 200 205

Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala  
 210 215 220

Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly  
 225 230 235 240

Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu  
 245 250 255

Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala  
 260 265 270



Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val  
 275 280 285

Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val  
 290 295 300

Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser  
 305 310 315 320

Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile.  
 325 330 335

Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly  
 340 345 350

Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His  
 355 360 365

Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys  
 370 375 380

Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp  
 385 390 395 400

Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met  
 405 410 415

Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln  
 420 425 430

Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile  
 435 440 445

Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr  
 450 455 460

Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu  
 465 470 475 480

Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr  
 485 490 495

Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val  
 500 505 510

Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala  
 515 520 525

Phe Glu Phe Leu Gln Thr Asn Val Val Arg  
 530 535

<210> 47

<211> 1332

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1332)

<223> 31895

<400> 47

atg tcg ata acg tac tcc gct att tcc tct agt aca gtt tct ggg ttt	48
Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe	
1 5 10 15	
tca cca aaa agt gta cct ttt gct att cat agc gta acc agg agg caa	96
Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln	
20 25 30	
ttt ctt aat ccc aac acg ttt tat aga ttt ggg ttc tct cct tct ctt	144
Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu	
35 40 45	
cag gga agt agc att gag ttt agc ctt cag ttg aat tca aga gtt gtg	192
Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val	
50 55 60	
ctt agt aaa gag cgt cga tct ctg cca tta gtt gtg aga aat gat cgt	240
Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg	
65 70 75 80	
cct cag aat gaa gac tta cct aag cag tac aca agg cga gag aag aaa	288
Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys	
85 90 95	
cct ttc cca gtc cct att gtg gac ctg aga cga gct gcg agg gag aga	336
Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg	
100 105 110	
gtc aag aac aac aaa gac aaa cct aag aga cct cta cct ccg cct aaa	384

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys	
115 120 125	
aat ggt atg gtt gtg aag agc ctt gtg cct ctt gct tat aaa gta tac	432
Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr	
130 135 140	
aat gca aga atc aga ttg atc aac aat ctc cac cgg ctt atg aaa gtt	480
Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val	
145 150 155 160	
gtt cgt gtt aat gct tgt ggg tgg tgc aat gag att cat gtt gga cct	528
Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro	
165 170 175	
tat ggg cat cca ttt aag tgc tgt aaa ggt ccc aat act tcc caa agg	576
Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg	
180 185 190	
aaa ggt ctt cat gaa tgg act aac tgc gtt att gag gac gtt att gtt	624
Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val	
195 200 205	
cct ctt gaa gcc tat cac ctt ttt gac cgc ctt ggc aag cgt atc cgt	672
Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg	
210 215 220	
cat gat gaa aga ttc tgc att ccc cga gtt cct gct gta gtt gag ctc	720
His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu	
225 230 235 240	
tgc att cag ggc ggc gtt gaa ata ccc gaa ttt cca gca aaa agg aga	768
Cys Ile Gln Gly Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg	
245 250 255	
aga aaa ccg att atc cgc att ggc aaa agc gag ttt gtt gat gca gat	816
Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp	
260 265 270	
gaa act gaa ttg cct gat cca gag cct cag cct cct cca gtg cca ttg	864
Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Pro Val Pro Leu	
275 280 285	
tta act gag tta cct gtc tca gag atc act ccc cca tct agc gaa gaa	912
Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu	
290 295 300	
gaa aca gtc tcc tta gcc gaa gaa aca tta cag gcc tgg gaa gaa atg	960
Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met	
305 310 315 320	
aga gca gga gcc aaa aag ctg atg agg atg tac agg gtt agg gtc tgt	1008
Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys	
325 330 335	
ggg tac tgt cca gag gtt cac gta ggt cca acg gga cac aag gcc cag	1056
Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln	
340 345 350	
aac tgt ggt gca ttc aag cac caa cag cgg aat ggc cag cat ggt tgg	1104

Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp  
 355 360 365  
 caa tct gca gta ctt gac gac ttg ata ccg cca aga tat gtt tgg cat 1152  
 Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His  
 370 375 380  
 gtt cct gat gtg aat ggg cca cag atg cag cga gag cta cga agc ttc 1200  
 Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe  
 385 390 395 400  
 tac ggg caa gca cct gct gtt gtg gag ata tgt gct cag gct ggc gct 1248  
 Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala  
 405 410 415  
 gtt gta cct gag cat tat aga gct aca atg aga ctg gag gtt gga att 1296  
 Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile  
 420 425 430  
 cct tcg agt gtg aaa gaa gct gag atg gtt gtt tga 1332  
 Pro Ser Ser Val Lys Glu Ala Glu Met Val Val  
 435 440

&lt;210&gt; 48

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe  
 1 5 10 15

Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln  
 20 25 30

Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu  
 35 40 45

Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val  
 50 55 60

Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg  
 65 70 75 80

Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys  
 85 90 95

Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg  
 100 105 110

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys  
 115 120 125

Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr  
 130 135 140

Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val  
 145 150 155 160

Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro  
 165 170 175

Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg  
 180 185 190

Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val  
 195 200 205

Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg  
 210 215 220

His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu  
 225 230 235 240

Cys Ile Gln Gly Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg  
 245 250 255

Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp  
 260 265 270

Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Pro Val Pro Leu  
 275 280 285

Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu  
 290 295 300

Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met  
 305 310 315 320

Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys  
 325 330 335

Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln  
 340 345 350

Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp  
 355 360 365

Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His  
 370 375 380

Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe  
 385 390 395 400

Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala  
 405 410 415

Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile  
 420 425 430

Pro Ser Ser Val Lys Glu Ala Glu Met Val Val  
 435 440

<210> 49

<211> 540

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (540)

<223> 34269

<400> 49

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 Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln  
 1 5 10 15

tgt tgt tgt ttg aga gag atg atg gct gcg aag ctt cag aaa tgg cga 96  
 Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg  
 20 25 30

aat ctg gca ggt cgt cta gat ctg atg aat cgg agc ggc gct gtg tcg 144  
 Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser  
 35 40 45

acg agg cgg ttc ctg cac gaa ggt cca gat acc gtg gag gag ctt ctc 192  
 Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu  
 50 55 60

gaa aga cat cta gcg aag aaa gag aaa cca ata atc gat cac gat gag 240  
 Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu  
 65 70 75 80

gct gag ttt ctg aat aga cgg cgt ctg acg agc acg cgc cgg gaa gcg 288  
 Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala  
 85 90 95

ttg agt ttg tac aga gac ata tta cga gcg act cgg ttc ttc acg tgg 336  
 Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp  
 100 105 110

att gat tcc agg gga aat tta tgg agg gac gtg ttg aga gag aac gcg 384  
 Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala  
 115 120 125

agg aag gag ttt gaa gcg gcg cga ttt gag acg gat ccg gag gtt atc 432  
 Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile  
 130 135 140

aca agg ctt ctg ata ggt gga agc gac gcc gtt tcg tct gct tta gat 480  
 Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp  
 145 150 155 160

aag ctt gcg gag aag caa aga gag atg att gag aaa caa cgc cgt ggt 528  
 Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly  
 165 170 175

gat caa cgc tga 540  
 Asp Gln Arg

&lt;210&gt; 50

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 50

Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln  
 1 5 10 15

Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg  
 20 25 30

Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser  
 35 40 45

Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu  
 50 55 60  
 Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu  
 65 70 75 80  
 Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala  
 85 90 95  
 Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp  
 100 105 110  
 Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala  
 115 120 125  
 Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile  
 130 135 140  
 Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp  
 145 150 155 160  
 Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly  
 165 170 175  
 Asp Gln Arg

<210> 51

<211> 708

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(708)

<223> 34540

<400> 51

atg aga tcc cct aga acc ttg gag gtt tgg aag cta ggc act gtc aac

48



Met	Arg	Ser	Pro	Arg	Thr	Leu	Glu	Val	Trp	Lys	Leu	Gly	Thr	Val	Asn		
1				5					10					15			
tat	ttg	aaa	tcc	ctt	aaa	ctg	cag	gag	aaa	tta	gtt	tca	gag	aga	aaa		96
Tyr	Leu	Lys	Ser	Leu	Lys	Leu	Gln	Glu	Lys	Leu	Val	Ser	Glu	Arg	Lys		
			20					25					30				
gct	cat	cag	att	cca	gat	acc	ctc	ctc	tcg	ctt	cag	cat	cca	cca	act		144
Ala	His	Gln	Ile	Pro	Asp	Thr	Leu	Leu	Ser	Leu	Gln	His	Pro	Pro	Thr		
			35				40					45					
tat	acg	ctc	gga	aag	cgt	aga	acc	gat	cac	aat	cta	ctt	atc	cct	gaa		192
Tyr	Thr	Leu	Gly	Lys	Arg	Arg	Thr	Asp	His	Asn	Leu	Leu	Ile	Pro	Glu		
	50					55					60						
tct	gaa	ctt	aca	aaa	atc	gga	gct	gaa	ctt	cat	tat	act	caa	aga	gga		240
Ser	Glu	Leu	Thr	Lys	Ile	Gly	Ala	Glu	Leu	His	Tyr	Thr	Gln	Arg	Gly		
65					70					75				80			
gga	gac	atc	acc	ttc	cat	ggc	cct	cat	caa	gcc	atc	tta	tat	ccc	atc		288
Gly	Asp	Ile	Thr	Phe	His	Gly	Pro	His	Gln	Ala	Ile	Leu	Tyr	Pro	Ile		
				85				90						95			
att	tcc	tta	cgc	agc	att	ggt	ttt	ggt	gct	agg	aac	tac	gtg	gag	aca		336
Ile	Ser	Leu	Arg	Ser	Ile	Gly	Phe	Gly	Ala	Arg	Asn	Tyr	Val	Glu	Thr		
			100				105						110				
ttg	gag	cgg	tca	atg	atc	gag	ttt	gct	tcg	att	tat	ggc	gtg	aaa	gct		384
Leu	Glu	Arg	Ser	Met	Ile	Glu	Phe	Ala	Ser	Ile	Tyr	Gly	Val	Lys	Ala		
		115				120						125					
cga	gca	gga	aac	aaa	tgt	gag	act	ggg	gtt	tgg	gtt	ggg	gat	agg	aag		432
Arg	Ala	Gly	Asn	Lys	Cys	Glu	Thr	Gly	Val	Trp	Val	Gly	Asp	Arg	Lys		
	130					135					140						
atc	ggt	gct	att	ggg	gtt	agg	ata	tct	tct	gga	atc	act	agt	cat	ggt		480
Ile	Gly	Ala	Ile	Gly	Val	Arg	Ile	Ser	Ser	Gly	Ile	Thr	Ser	His	Gly		
145					150					155					160		
ttg	gcc	tta	aat	ata	gat	cct	gat	atg	aag	tac	ttt	gag	cac	att	gtg		528
Leu	Ala	Leu	Asn	Ile	Asp	Pro	Asp	Met	Lys	Tyr	Phe	Glu	His	Ile	Val		
				165				170						175			
cct	tgt	ggg	att	gct	gat	aaa	gaa	gtt	aca	tct	ttg	cga	aga	gag	acg		576
Pro	Cys	Gly	Ile	Ala	Asp	Lys	Glu	Val	Thr	Ser	Leu	Arg	Arg	Glu	Thr		
			180					185					190				
gat	act	ctg	ctt	cct	tca	gaa	gaa	gtg	att	cat	gaa	cag	ttg	gtt	tct		624
Asp	Thr	Leu	Leu	Pro	Ser	Glu	Glu	Val	Ile	His	Glu	Gln	Leu	Val	Ser		
			195			200						205					
tgt	tta	gcc	aaa	gcg	ttt	tct	tat	gat	gat	gtt	gtc	tgg	aag	gaa	gat		672
Cys	Leu	Ala	Lys	Ala	Phe	Ser	Tyr	Asp	Asp	Val	Val	Trp	Lys	Glu	Asp		
	210				215						220						
cct	tca	ctc	att	ttg	gac	acc	caa	gat	aaa	gaa	taa						708
Pro	Ser	Leu	Ile	Leu	Asp	Thr	Gln	Asp	Lys	Glu							
225					230					235							

&lt;210&gt; 52

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 52

Met Arg Ser Pro Arg Thr Leu Glu Val Trp Lys Leu Gly Thr Val Asn  
 1 5 10 15

Tyr Leu Lys Ser Leu Lys Leu Gln Glu Lys Leu Val Ser Glu Arg Lys  
 20 25 30

Ala His Gln Ile Pro Asp Thr Leu Leu Ser Leu Gln His Pro Pro Thr  
 35 40 45

Tyr Thr Leu Gly Lys Arg Arg Thr Asp His Asn Leu Leu Ile Pro Glu  
 50 55 60

Ser Glu Leu Thr Lys Ile Gly Ala Glu Leu His Tyr Thr Gln Arg Gly  
 65 70 75 80

Gly Asp Ile Thr Phe His Gly Pro His Gln Ala Ile Leu Tyr Pro Ile  
 85 90 95

Ile Ser Leu Arg Ser Ile Gly Phe Gly Ala Arg Asn Tyr Val Glu Thr  
 100 105 110

Leu Glu Arg Ser Met Ile Glu Phe Ala Ser Ile Tyr Gly Val Lys Ala  
 115 120 125

Arg Ala Gly Asn Lys Cys Glu Thr Gly Val Trp Val Gly Asp Arg Lys  
 130 135 140

Ile Gly Ala Ile Gly Val Arg Ile Ser Ser Gly Ile Thr Ser His Gly  
 145 150 155 160

Leu Ala Leu Asn Ile Asp Pro Asp Met Lys Tyr Phe Glu His Ile Val  
 165 170 175

Pro Cys Gly Ile Ala Asp Lys Glu Val Thr Ser Leu Arg Arg Glu Thr  
 180 185 190

Asp Thr Leu Leu Pro Ser Glu Glu Val Ile His Glu Gln Leu Val Ser  
 195 200 205

Cys Leu Ala Lys Ala Phe Ser Tyr Asp Asp Val Val Trp Lys Glu Asp  
 210 215 220

Pro Ser Leu Ile Leu Asp Thr Gln Asp Lys Glu  
 225 230 235

<210> 53

<211> 1473

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1473)

<223>

<400> 53

atg cag aca ttt tca att tca ctc ctc cgt cac tct tct ccg ttc ctc 48  
 Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu  
 1 5 10 15

cgt cac acc gcg att ttt cac ggc gga gtt gga gtt aga ttc aaa ttc 96  
 Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe  
 20 25 30

ctt cgc agc ttt tct cct ctc tca gca aga cga gat aat ccc gat gtc 144  
 Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val  
 35 40 45

tcc aga aaa ccc caa ccg agc aaa aat atg ctc aga gcg aag cac atc 192  
 Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile  
 50 55 60

ggg aaa aat tac tcc tcc tcc ttg tca cca gtt ctc tcg ccg gag cat 240  
 Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His  
 65 70 75 80

aaa cct tcg ctc tta gag tct caa gct att ggt act gtc gca aca gct 288  
 Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala  
 85 90 95

caa gcg aac ttt atg cgc gtc att gtt caa gat gta gct aat tct gtg 336  
 Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val  
 100 105 110

acg agt gat gat gat aat gat tct tca aag act ggt gtt gaa ttg ctt 384  
 Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu  
 115 120 125

tgt gtg gtg aga gct gtg ttg aag aaa ata cga agg aga gtt tta gtt 432  
 Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val  
 130 135 140

gga gat aag gtt ctt gtt gga tct att gat tgg gtt gat aga aga gga 480  
 Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly  
 145 150 155 160

atg att gag aat gtg ttt cat cga cgt tct gag att ttg gat cca cct 528  
 Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro  
 165 170 175

gtt gcg aac gtt gat cat ttg ctt gtt ctt ttc tct ttg gat caa ccg 576  
 Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro  
 180 185 190

aaa ctt gag ccg ttt act ctt act agg ttc ttg gtg gaa gct gaa tct 624  
 Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser  
 195 200 205

act cgt att cca tta aca ctt gct ttg aat aaa act gaa ctc att agt 672  
 Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser  
 210 215 220

gaa gag gaa ttg gaa act tgg aag ata agg ttg cgt gga tgg aac tat 720  
 Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr  
 225 230 235 240

gaa cca ttg ttt tgt agt gtg gga act aaa gat gga ctt gat gat att 768  
 Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Ile  
 245 250 255

gcg ttt gtt ctg aga gat cag act tct gtg att gtt gga cct agt ggt 816  
 Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly  
 260 265 270

gtt gga aag tct agt tta atc aac gta ttg agg agt aat cat ggt ggt 864  
 Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly  
 275 280 285

ggt gtg gtg gaa gat gag aat tgg ttt gag cct atg tta ggt aat aag 912  
 Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys  
 290 295 300

tgg ttt gat gat cag cga gta ggg gaa gtt tct agt aga agt ggt aga 960  
 Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg  
 305 310 315 320

ggt aaa cat aca aca cga aat gta tct cta ctg ccg gtt tct gaa ggt 1008  
 Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly  
 325 330 335

ggt tac ctc gct gat act cct ggc ttt aac cag cct agt ttg ctg aaa 1056  
 Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys  
 340 345 350

gta acg aag cat tca cta gct cac tgt ttt cct gag ata cgg aac atg 1104  
Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met  
355 360 365

att gag agc gaa aaa tgt gga ttc aga gac tgc ttg cat att ggg gaa 1152  
Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu  
370 375 380

cca gga tgt gtt gtg aaa ggt gac tgg gaa agg tat cct tac tac tta 1200  
Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu  
385 390 395 400

caa ttg ctt gat gag atc aga atc agg gaa gaa ttt cag ctt agg act 1248  
Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr  
405 410 415

ttt gga acc aaa agg gaa gat gat gtt agg tac aag gtg gga gac atg 1296  
Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met  
420 425 430

ggt gtg aaa cat gct gaa cca cgg tta atg cct aag aag cat agg aga 1344  
Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg  
435 440 445

gag tca agg aag aaa acg aaa cag aca atg atc agt gag ctg gat gag 1392  
Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu  
450 455 460

ttc gaa gat gaa gac agt gat ttg tac ata gag aac gac cca atc gtc 1440  
Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val  
465 470 475 480

caa gcc att gag aat gag aat aaa aga caa tga 1473  
Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln  
485 490

&lt;210&gt; 54

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 54

Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu  
1 5 10 15

Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe  
20 25 30

Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val  
35 40 45

Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile  
 50 55 60

Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His  
 65 70 75 80

Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala  
 85 90 95

Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val  
 100 105 110

Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu  
 115 120 125

Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val  
 130 135 140

Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly  
 145 150 155 160

Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro  
 165 170 175

Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro  
 180 185 190

Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser  
 195 200 205

Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser  
 210 215 220

Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr  
 225 230 235 240

Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile  
 245 250 255

Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly  
 260 265 270

Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly  
 275 280 285

Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys  
 290 295 300

Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg  
 305 310 315 320

Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly  
 325 330 335

Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys  
 340 345 350

Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met  
 355 360 365

Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu  
 370 375 380

Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu  
 385 390 395 400

Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr  
 405 410 415

Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met  
 420 425 430

Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg  
 435 440 445

Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu  
 450 455 460

Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val  
 465 470 475 480

Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln  
 485 490

<210> 55

<211> 897

&lt;212&gt; DNA

<213> *Arabidopsis thaliana*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(897)

&lt;223&gt; 35154

&lt;400&gt; 55

atg	gtg	ttt	gga	caa	gta	gta	ata	ggg	cct	cca	gga	tcg	gga	aag	acc	48
Met	Val	Phe	Gly	Gln	Val	Val	Ile	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	
1			5					10						15		
act	tat	tgc	aat	gga	atg	tct	cag	ttc	ctc	tct	cta	atg	ggc	agg	aag	96
Thr	Tyr	Cys	Asn	Gly	Met	Ser	Gln	Phe	Leu	Ser	Leu	Met	Gly	Arg	Lys	
			20				25						30			
gtt	gct	att	gtt	aat	ctg	gat	cct	gca	aat	gat	gca	tta	cct	tat	gag	144
Val	Ala	Ile	Val	Asn	Leu	Asp	Pro	Ala	Asn	Asp	Ala	Leu	Pro	Tyr	Glu	
			35				40					45				
tgt	ggg	gtg	aat	ata	gaa	gaa	ttg	atc	aag	tta	gaa	gat	gtt	atg	tcg	192
Cys	Gly	Val	Asn	Ile	Glu	Glu	Leu	Ile	Lys	Leu	Glu	Asp	Val	Met	Ser	
	50					55					60					
gaa	cac	tcg	ctt	ggg	cct	aat	gga	ggg	ctt	gta	tat	tgt	atg	gag	tac	240
Glu	His	Ser	Leu	Gly	Pro	Asn	Gly	Gly	Leu	Val	Tyr	Cys	Met	Glu	Tyr	
65					70				75					80		
ttg	gag	aaa	aac	att	gac	tgg	ctg	gaa	tct	aaa	cta	aag	cct	ctt	ctg	288
Leu	Glu	Lys	Asn	Ile	Asp	Trp	Leu	Glu	Ser	Lys	Leu	Lys	Pro	Leu	Leu	
			85				90							95		
aag	gat	cat	tac	att	ctc	ttt	gat	ttt	cct	ggc	caa	gtg	gaa	ttg	ttc	336
Lys	Asp	His	Tyr	Ile	Leu	Phe	Asp	Phe	Pro	Gly	Gln	Val	Glu	Leu	Phe	
			100				105						110			
ttc	att	cat	gac	agt	acc	aag	aat	gtt	ctc	acg	aag	ctg	att	aaa	tca	384
Phe	Ile	His	Asp	Ser	Thr	Lys	Asn	Val	Leu	Thr	Lys	Leu	Ile	Lys	Ser	
			115				120						125			
ttg	aac	ctt	aga	tta	act	gct	gtg	caa	cta	att	gat	tcc	cat	cta	tgt	432
Leu	Asn	Leu	Arg	Leu	Thr	Ala	Val	Gln	Leu	Ile	Asp	Ser	His	Leu	Cys	
			130			135					140					
tgt	gat	ccc	ggg	aac	tac	gta	agt	tcg	cta	ctt	ctc	tcc	tta	tcc	aca	480
Cys	Asp	Pro	Gly	Asn	Tyr	Val	Ser	Ser	Leu	Leu	Leu	Ser	Leu	Ser	Thr	
145				150					155					160		
atg	ctt	cac	atg	gaa	ctc	cca	cat	gtc	aat	gta	ttg	tct	aaa	atc	gat	528
Met	Leu	His	Met	Glu	Leu	Pro	His	Val	Asn	Val	Leu	Ser	Lys	Ile	Asp	
				165				170						175		



ctg att gga agc tac ggg aag cta gct ttc aat tta gat ttc tat acc 576  
 Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr  
 180 185 190

gat gtt caa gac ttg tca tac ttg gag cac cat ctt agt caa gat cct 624  
 Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro  
 195 200 205

cgc tct gct aag tac aga aaa cta aca aaa gag cta tgt agt gtc att 672  
 Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile  
 210 215 220

gaa gat tac agt ctt gtt aat ttt aca acc ttg gat att cag gat aaa 720  
 Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys  
 225 230 235 240

gaa agt gtt ggg gat cta gta aag ctc atc gac aag agc aat gga tac 768  
 Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr  
 245 250 255

ata ttt gcc ggc att gat gca agt gtg gtt gaa tac agc aag att gca 816  
 Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala  
 260 265 270

att ggt caa act gat tgg gat tat aac aga gtc gca gct gta cag gag 864  
 Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu  
 275 280 285

aag tac atg gaa gat gag gaa ata caa gac tga 897  
 Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp  
 290 295

&lt;210&gt; 56

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 56

Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr  
1 5 10 15

Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys  
20 25 30

Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu  
35 40 45

Cys Gly Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser  
50 55 60

Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr  
 65 70 75 80  
 Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu  
 85 90 95  
 Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe  
 100 105 110  
 Phe Ile His Asp Ser Thr Lys Asn Val Leu Thr Lys Leu Ile Lys Ser  
 115 120 125  
 Leu Asn Leu Arg Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys  
 130 135 140  
 Cys Asp Pro Gly Asn Tyr Val Ser Ser Leu Leu Leu Ser Leu Ser Thr  
 145 150 155 160  
 Met Leu His Met Glu Leu Pro His Val Asn Val Leu Ser Lys Ile Asp  
 165 170 175  
 Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr  
 180 185 190  
 Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro  
 195 200 205  
 Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile  
 210 215 220  
 Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys  
 225 230 235 240  
 Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr  
 245 250 255  
 Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala  
 260 265 270  
 Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu  
 275 280 285  
 Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp  
 290 295

&lt;210&gt; 57

&lt;211&gt; 849

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (849)

&lt;223&gt; 35438

&lt;400&gt; 57

atg gaa gct ctc tac gcc aag ctc tac gac aaa tac acc aaa ctc cag	48
Met Glu Ala Leu Tyr Ala Lys Leu Tyr Asp Lys Tyr Thr Lys Leu Gln	
1 5 10 15	

aag aag aaa tat tcc gaa tac gat gag att aat aag gaa caa gaa gag	96
Lys Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu	
20 25 30	

aaa ttc ctt acc ttt gtt tca gcc tca gag gag ttg atg gaa cat ttg	144
Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu	
35 40 45	

aga ggt gaa aat cag agt tct ctg gag atg gtt gag aag ttg agg aat	192
Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn	
50 55 60	

gaa atc att tca atc aga tct ggc agg gac gac aag ttt ctg gag tgt	240
Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys	
65 70 75 80	

caa aag ctt ctc atg gaa gaa gaa cta aag aac aaa tca ctt tct gaa	288
Gln Lys Leu Leu Met Glu Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu	
85 90 95	

gaa gtt gtc aag cta aaa gag ctg gtc caa gag gaa cat cct cgc aac	336
Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn	
100 105 110	

tat gaa gat caa agt gga aaa aaa caa aag aga aag act cct gaa agt	384
Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser	
115 120 125	

gct cga gtt aca acg aga agc atg ata aaa cgt agc aga ctg tca gaa	432
Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu	
130 135 140	

gat ttg gtg gaa acg gat atg gta tca cct gac att agc aaa cat cat	480
---	-----

Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His  
 145 150 155 160  
 aaa gca aag gag cct ctc ttg gtt tct cag cca caa tgc tgc aga aca 528  
 Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr  
 165 170 175  
 acc tac gat gga tca agt agt tct gct agt tgt aca ttt caa gct ctt 576  
 Thr Tyr Asp Gly Ser Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu  
 180 185 190  
 ggc aaa cac ttg cta gga atg aaa tta tca act aat aat aag ggc aaa 624  
 Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys  
 195 200 205  
 cgc gcc tgc att gta gcc tca cac cca aca acc ggt tta tcc ttc agc 672  
 Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser  
 210 215 220  
 cta act ttt ata aat aac cca aat ggt gaa gaa tct gag ctg ctt tac 720  
 Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Glu Ser Glu Leu Leu Tyr  
 225 230 235 240  
 aag cct gca tca ctc gga aca ttt caa aga gtg gca ccg gaa tgg atg 768  
 Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met  
 245 250 255  
 aga gaa gtt ata aag ttc agc aca agt atg tgt ccc atc ttc ttt gaa 816  
 Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu  
 260 265 270  
 aga gtc tct cga gtc att aag ctc aat tgt tga 849  
 Arg Val Ser Arg Val Ile Lys Leu Asn Cys  
 275 280

&lt;210&gt; 58

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 58

Met Glu Ala Leu Tyr Ala Lys Leu Tyr Asp Lys Tyr Thr Lys Leu Gln  
 1 5 10 15

Lys Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu  
 20 25 30

Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu  
 35 40 45

Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn  
 50 55 60

Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys  
 65 70 75 80

Gln Lys Leu Leu Met Glu Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu  
 85 90 95

Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn  
 100 105 110

Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser  
 115 120 125

Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu  
 130 135 140

Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His  
 145 150 155 160

Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr  
 165 170 175

Thr Tyr Asp Gly Ser Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu  
 180 185 190

Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys  
 195 200 205

Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser  
 210 215 220

Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Glu Ser Glu Leu Leu Tyr  
 225 230 235 240

Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met  
 245 250 255

Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu  
 260 265 270

Arg Val Ser Arg Val Ile Lys Leu Asn Cys  
 275 280

&lt;210&gt; 59

&lt;211&gt; 1467

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1467)

&lt;223&gt; 37351

&lt;400&gt; 59

atg gaa ttg gat tcg gag aac aaa ttg ttg aag acg ggt ttg gtt ata	48
Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile	
1 5 10 15	
gtg gcg aca ctt gtt ata gcc aaa ctc atc ttc tct ttc ttc act tct	96
Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser	
20 25 30	
gat tct aag aag aag cgt ctt cct cct act ctt aaa gct tgg cct cca	144
Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro	
35 40 45	
ttg gtt gga agt ctt atc aaa ttc ttg aaa gga cct att att atg ctt	192
Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu	
50 55 60	
aga gag gaa tac cct aag ctt gga agt gtg ttt act gtt aat ctt gtt	240
Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val	
65 70 75 80	
cac aaa aag att act ttt ctt att ggt cct gaa gtc tct gct cat ttt	288
His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe	
85 90 95	
ttc aaa gct tct gaa tct gat ctt agt cag cag gaa gtg tat cag ttc	336
Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe	
100 105 110	
aat gtc cct act ttt ggt cct gga gtt gtt ttc gat gtt gat tat tct	384
Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser	
115 120 125	
gtt cgt cag gag cag ttt cgg ttc ttc act gag gca ctt aga gtt aac	432
Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn	
130 135 140	
aag ttg aag ggt tat gtg gat atg atg gtt act gaa gct gag gat tac	480
Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr	
145 150 155 160	

ttc tct aaa tgg gga gag agt ggt gaa gtt gat att aag gtt gag cta Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu 165 170 175	528
gag agg ctc atc atc ttg act gca agt aga tgt tta ctg ggt cga gaa Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu 180 185 190	576
gtt cgt gat cag ctt ttt gat gat gtc tct gct ttg ttc cat gac ctt Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu 195 200 205	624
gac aat gga atg ctt ccc atc agt gtt ctc ttc cca tat ctc cca att Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile 210 215 220	672
cca gct cac cgc cgt cgt gac cgt gcc cga gaa aag ctt tcg gag att Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile 225 230 235 240	720
ttc gca aaa atc att ggg tcg aga aaa cgc tct gga aaa aca gag aac Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn 245 250 255	768
gac atg ctg cag tgt ttc atc gaa tca aag tac aaa gat ggt aga cag Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln 260 265 270	816
aca acc gaa tct gaa gtc act ggt ttg ctc att gct gct ctg ttt gca Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala 275 280 285	864
gga caa cac acg agc tct atc act tcc acc tgg acc ggt gct tat ctg Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu 290 295 300	912
atg cga tac aaa gag tac ttc tca gct gct ctt gat gag cag aag aac Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn 305 310 315 320	960
ctg att gcg aaa cat gga gac aag atc gat cat gat atc tta tcc gag Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu 325 330 335	1008
atg gat gtt ctc tac cgc tgc att aag gaa gcg ttg agg ctt cac cct Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro 340 345 350	1056
cca ctc atc atg tta atg aga gcc tcg cac agt gat ttc agc gtg aca Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr 355 360 365	1104
gct cgg gat gga aaa act tac gat atc cca aag ggt cac atc gtt gca Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala 370 375 380	1152
acc tcc cct gca ttt gcc aac cgc tta ccg cac atc ttc aaa gac ccc Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro 385 390 395 400	1200

gac acc tac gac cca gaa aga ttc tcc cct gga aga gaa gag gac aaa 1248  
 Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys  
 405 410 415  
 gcc gca ggg gca ttc tcg tac att gca ttc gga ggg gga agg cac ggg 1296  
 Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly  
 420 425 430  
 tgc ctt gga gag ccg ttt gct tac ctg cag atc aaa gcc ata tgg agt 1344  
 Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser  
 435 440 445  
 cat ttg ttg agg aac ttc gag ctt gag cta gtt tca ccg ttc cct gag 1392  
 His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu  
 450 455 460  
 att gac tgg aac gct atg gtg gtt gga gtt aaa ggc aat gtg atg gtg 1440  
 Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val  
 465 470 475 480  
 cgt tac aag agg cgc cag ctt tct taa 1467  
 Arg Tyr Lys Arg Arg Gln Leu Ser  
 485

&lt;210&gt; 60

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 60

Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile  
 1 5 10 15

Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser  
 20 25 30

Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro  
 35 40 45

Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu  
 50 55 60

Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val  
 65 70 75 80

His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe  
 85 90 95



Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe  
 100 105 110

Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser  
 115 120 125

Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn  
 130 135 140

Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr  
 145 150 155 160

Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu  
 165 170 175

Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu  
 180 185 190

Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu  
 195 200 205

Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile  
 210 215 220

Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile  
 225 230 235 240

Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn  
 245 250 255

Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln  
 260 265 270

Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala  
 275 280 285

Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu  
 290 295 300

Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn  
 305 310 315 320

Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu  
 325 330 335

Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro  
                   340                                  345                                  350

Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr  
                   355                                  360                                  365

Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala  
                   370                                  375                                  380

Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro  
                   385                                  390                                  395                                  400

Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys  
                                   405                                  410                                  415

Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly  
                                   420                                  425                                  430

Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser  
                                   435                                  440                                  445

His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu  
                                   450                                  455                                  460

Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val  
                   465                                  470                                  475                                  480

Arg Tyr Lys Arg Arg Gln Leu Ser  
                                   485

<210> 61

<211> 1836

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1836)

<223> 37389

<400> 61  
 atg ggg att gtt ttg gaa cct cct tgt cct aaa agt gtt gat ggg att 48  
 Met Gly Ile Val Leu Glu Pro Pro Cys Pro Lys Ser Val Asp Gly Ile  
 1 5 10 15

agc att gat cct gag cct aat tgg aat ttc gag agt ttg gtc gct gag 96  
 Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu  
 20 25 30

att gct tct gtt gaa aag aag ctc aat ggc ttc tca atg tat cct cag 144  
 Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln  
 35 40 45

cca att act aac aca acc tta cgg atg gga agg aga ggt gga gga ttt 192  
 Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Gly Phe  
 50 55 60

gta atg cat gtc tca gaa gat gag atg gag agt gac gaa ggt gaa gag 240  
 Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu  
 65 70 75 80

agt gat gat gag gaa gaa gaa gaa gat cat agt caa atc tgt aca gcg 288  
 Ser Asp Asp Glu Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala  
 85 90 95

gga aaa cgt ttt gcc tgt gat gag ctt tac ttg agt gat gaa tct gat 336  
 Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp  
 100 105 110

gaa gag ttt gat cat gaa cct gag tat atg atg aat aag ttg ggt ctg 384  
 Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu  
 115 120 125

gct gag agt gcc cta tat gag gtt atc aac gac cac caa acc gaa atc 432  
 Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile  
 130 135 140

aag gac gac att agg aat caa gta tca gtt gtt gaa aca gaa ata atg 480  
 Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met  
 145 150 155 160

aat gag att gaa acg tct ctc tct gcc ata gcc cgg gtt gaa aag tac 528  
 Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr  
 165 170 175

agt gag act cgg aaa gaa gtt gaa cgg aaa ctt gat ctt caa tat cag 576  
 Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln  
 180 185 190

cga aaa gtt gct gaa gca ctt gat acc cat ctg act gca gtc caa cgc 624  
 Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg  
 195 200 205

gaa cat aaa att aaa tcg caa ata gaa gaa aga aag ata agg agc gag 672  
 Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu  
 210 215 220

gaa gct cag gag gag gcc agg agg aag gaa agg gct cat caa gaa gag 720

Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu	
225 230 235 240	
aaa ata cgt caa gaa aaa gct cgc gca gag gct caa atg cta gca aaa	768
Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys	
245 250 255	
atc aga gct gaa gaa gaa aag aaa gaa gtt gag aga aag gca gcc aga	816
Ile Arg Ala Glu Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg	
260 265 270	
gaa gta gct gaa aaa gaa gta gca gat cgc aaa gct gcc gaa caa aaa	864
Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys	
275 280 285	
ctt gcg gaa cag aag gct gtg ata gag agt gtt acg ggg agt tca gct	912
Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala	
290 295 300	
aca tca aat gct caa gct ggg ggt aat tca atc cga gct gca gaa agt	960
Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser	
305 310 315 320	
gct ttg ata ttg gag aac cac aga ttg aaa aag ctc gaa gaa cta gaa	1008
Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu	
325 330 335	
aca acg aac caa tcg ctt aag tca cgt tca aat gaa aac ttt agc agt	1056
Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser	
340 345 350	
ttt gag aag cat att gga aga gtg ata agg caa ata agt ggg aca aag	1104
Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys	
355 360 365	
gat agt gta agt ggg aaa atc aat gat att gtg aaa ata ttt aaa gac	1152
Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp	
370 375 380	
cct cgt tgt ccg gta tcc ata agt att gca gct ttt gca aag aag atg	1200
Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met	
385 390 395 400	
gtc acc act aag gaa aaa cca aac cct ttt gca tgc agc tat gtc att	1248
Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile	
405 410 415	
gtt tac atc aac tca cag ttt ccc caa gtt atg gat att ctt ctc gcg	1296
Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala	
420 425 430	
gaa ttc cac aaa gct tgc att tac act gtc cca aag cat att gta aac	1344
Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn	
435 440 445	
tca cag tca gct tgg gat tca gac gca tat gaa cgc cta gat tct ata	1392
Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile	
450 455 460	
atg agg ctc tac ggt gca ctt gtt cag acc gat atc cgc gtt ggc aat	1440

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn  
 465 470 475 480

gct act aac gtt cat ggg ata gaa cat gga tgg gct tgg tta gcc cgg 1488  
 Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg  
 485 490 495

ttc ctt aac aaa atc cca gcc aac aga gcc act gcg aca gcc ttg aac 1536  
 Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn  
 500 505 510

tcc ttt ctc cag acg gct ggg ttt ggt ctt cat cag agg tac aaa tct 1584  
 Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser  
 515 520 525

cag ttt ctg aag gtt gtg aat gtt gtg aga gag cat ttc ttg cag aaa 1632  
 Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys  
 530 535 540

ttg cgg gcg aag aag gac acg tgc gat cta ctt gtg atc ata gcc gaa 1680  
 Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu  
 545 550 555 560

atc aca gcg tac tta gat gac cgg atg tat ctc aag gaa cct gaa gga 1728  
 Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly  
 565 570 575

aga gct atg aag acg act agt acc ttg tcc tct gaa ctt act gct gaa 1776  
 Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu  
 580 585 590

tta aat cag ccg aac tac aat cag aat tac cag agg aat gat tac aga 1824  
 Leu Asn Gln Pro Asn Tyr Asn Gln Asn Tyr Gln Arg Asn Asp Tyr Arg  
 595 600 605

aac tac tat tga 1836  
 Asn Tyr Tyr  
 610

&lt;210&gt; 62

&lt;211&gt; 611

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 62

Met Gly Ile Val Leu Glu Pro Pro Cys Pro Lys Ser Val Asp Gly Ile  
 1 5 10 15

Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu  
 20 25 30

Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln  
 35 40 45

Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Gly Phe  
 50 55 60

Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu  
 65 70 75 80

Ser Asp Asp Glu Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala  
 85 90 95

Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp  
 100 105 110

Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu  
 115 120 125

Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile  
 130 135 140

Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met  
 145 150 155 160

Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr  
 165 170 175

Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln  
 180 185 190

Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg  
 195 200 205

Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu  
 210 215 220

Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu  
 225 230 235 240

Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys  
 245 250 255

Ile Arg Ala Glu Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg  
 260 265 270

Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys  
 275 280 285

Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala  
 290 295 300

Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser  
 305 310 315 320

Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu  
 325 330 335

Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser  
 340 345 350

Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys  
 355 360 365

Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp  
 370 375 380

Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met  
 385 390 395 400

Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile  
 405 410 415

Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala  
 420 425 430

Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn  
 435 440 445

Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile  
 450 455 460

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn  
 465 470 475 480

Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg  
 485 490 495

Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn  
 500 505 510

Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser  
 515 520 525

Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys  
 530 535 540

Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu  
 545 550 555 560

Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly  
 565 570 575

Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu  
 580 585 590

Leu Asn Gln Pro Asn Tyr Asn Gln Asn Tyr Gln Arg Asn Asp Tyr Arg  
 595 600 605

Asn Tyr Tyr  
 610

<210> 63

<211> 1152

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1152)

<223> 38108

<400> 63

atg gca acg gct tct cct cca ttt atc tca act ctc agc ttc act cac  
 Met Ala Thr Ala Ser Pro Pro Phe Ile Ser Thr Leu Ser Phe Thr His  
 1 5 10 15

48

tct tct ttc aaa act tct tct tct tct tca ttt tct ccg aag ctt ctt  
 Ser Ser Phe Lys Thr Ser Ser Ser Ser Ser Phe Ser Pro Lys Leu Leu  
 20 25 30

96

cga ccc ctc tta agc ttt tcc gtc aaa gct tcc aga aag caa gta gag  
 Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu  
 35 40 45

144



ata gtg ttt gat cct gat gag agg ctt aat aag ata ggt gat gat gtt Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val 50 55 60	192
gac aaa gaa gct cct ttg tcc agg ctt aag ctc ttc tca cct tgc aag Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys 65 70 75 80	240
atc aat gtt ttc ttg agg atc acc gga aag cga gaa gat ggg ttt cat Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His 85 90 95	288
gat tta gcc tct ttg ttt cat gtg att agc tta gga gac act att aaa Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys 100 105 110	336
ttc tca ttg tca cca tca aag tct aaa gat cgt ttg tct act aac gtt Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val 115 120 125	384
caa gga gtc cct gtt gat ggg aga aat ctg att ata aaa gca ctt aac Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn 130 135 140	432
ctt tac agg aag aaa act ggt agt aac aga ttc ttc tgg att cat tta Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu 145 150 155 160	480
gat aag aag gtg cct acc ggg gct gga ctc ggt ggt gga agt agt aat Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Gly Ser Ser Asn 165 170 175	528
gct gca act gca ctc tgg gcg gca aat gag ctc aat gga ggt ctt gtc Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val 180 185 190	576
act gag aac gaa ctc cag gat tgg tca agt gaa att ggg tca gat att Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile 195 200 205	624
cct ttc ttc ttc tcg cat gga gct gcc tat tgt acc ggg aga ggt gag Pro Phe Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu 210 215 220	672
att gtc caa gac ctt cct cca cct ttt cct ctt gat ctt ccg atg gtg Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val 225 230 235 240	720
ctc ata aag ccc cga gaa gca tgt tcc act gct gaa gtt tac aaa cgt Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg 245 250 255	768
ctt cgt tta gat cag acg agc aat att aat ccc ttg aca tta cta gag Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu 260 265 270	816
aat gtg acc agc aat ggt gtg tct caa agc ata tgc gta aac gat ttg Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu 275 280 285	864

gaa ccg cca gcg ttt tca gtt ctt cca tct cta aaa cgc ttg aag caa 912  
 Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln  
 290 295 300

cgg ata ata gca tct gga cgt ggg gaa tac gat gct gtg ttt atg tct 960  
 Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser  
 305 310 315 320

ggg agt gga agc act att atc ggt att ggt tca cca gat cct cct caa 1008  
 Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln  
 325 330 335

ttt ata tat gat gat gaa gaa tac aag aac gtg ttc ttg tct gaa gca 1056  
 Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala  
 340 345 350

aac ttt atg acg cgt gag gct aat gaa tgg tac aaa gaa cct gct tct 1104  
 Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser  
 355 360 365

gca aat gct act acc tca tcc gcc gaa tct cgc atg gat ttc caa tga 1152  
 Ala Asn Ala Thr Thr Ser Ser Ala Glu Ser Arg Met Asp Phe Gln  
 370 375 380

&lt;210&gt; 64

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 64

Met Ala Thr Ala Ser Pro Pro Phe Ile Ser Thr Leu Ser Phe Thr His  
 1 5 10 15

Ser Ser Phe Lys Thr Ser Ser Ser Ser Ser Phe Ser Pro Lys Leu Leu  
 20 25 30

Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu  
 35 40 45

Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val  
 50 55 60

Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys  
 65 70 75 80

Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His  
 85 90 95

Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys  
 100 105 110

Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val  
 115 120 125

Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn  
 130 135 140

Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu  
 145 150 155 160

Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Gly Ser Ser Asn  
 165 170 175

Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val  
 180 185 190

Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile  
 195 200 205

Pro Phe Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu  
 210 215 220

Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val  
 225 230 235 240

Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg  
 245 250 255

Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu  
 260 265 270

Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu  
 275 280 285

Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln  
 290 295 300

Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser  
 305 310 315 320

Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln  
 325 330 335

Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala  
 340 345 350

Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser  
 355 360 365

Ala Asn Ala Thr Thr Ser Ser Ala Glu Ser Arg Met Asp Phe Gln  
 370 375 380

<210> 65

<211> 1152

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (1152)

<223> 43301

<400> 65

atg gag gag tca cga gaa tcg ccg gcg gaa cac ggc tac tac atg ccg 48  
 Met Glu Glu Ser Arg Glu Ser Pro Ala Glu His Gly Tyr Tyr Met Pro  
 1 5 10 15

gcg gaa tgg gat tct cat gct caa act tgg atc ggt tgg cct gaa cgg 96  
 Ala Glu Trp Asp Ser His Ala Gln Thr Trp Ile Gly Trp Pro Glu Arg  
 20 25 30

caa gat aac tgg cgg cac aac gct tta ccc gca caa cga gtg ttt gca 144  
 Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala  
 35 40 45

gat gtt gca aag gcc atc tca aag ttc gag cct gtc act gtc tgt gct 192  
 Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala  
 50 55 60

agc cct gct cag tgg gaa aat gca agg aaa cag ctt cca gag gat ata 240  
 Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile  
 65 70 75 80

aga gtt gtt gag atg agc atg aat gat tct tgg ttc cgc gac tct gga 288  
 Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly  
 85 90 95

cca act ttc att gta cgg aaa aga cca gta aag ctc agt tct ctt aac 336

Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn	
100 105 110	
cga aac att gct ggg atc gac tgg aat ttc aat gcc tgg gga gga gct	384
Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala	
115 120 125	
aat gat ggc tgt tac aat gat tgg agt cat gac ctt tta gtt tca cga	432
Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg	
130 135 140	
aag att ctc gct ttg gaa cga att cca aga ttt caa cat tcg atg att	480
Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile	
145 150 155 160	
ctt gaa gga ggc agc atc cat gtc gat ggg gaa gga acc tgc ctt gtc	528
Leu Glu Gly Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val	
165 170 175	
aca gaa gag tgt ctc ttg aac aaa aac cga aac cct cat atg agt aaa	576
Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys	
180 185 190	
gag caa ata gag gaa gaa ctt aag aag tac ctc gga gta caa tca ttt	624
Glu Gln Ile Glu Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe	
195 200 205	
atc tgg ctt cct cgt ggt ctt tac ggg gat gag gac aca aat ggt cac	672
Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His	
210 215 220	
att gat aac atg tgc tgc ttc gct aga ccg gga gtt gtg tta ttg tct	720
Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser	
225 230 235 240	
tgg aca gac gat gaa acc gat cct caa tac gaa agg tct gtg gaa gct	768
Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala	
245 250 255	
ctt tcg gtt ttg tcg aat tcg att gat gct cgt gga agg aag att caa	816
Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln	
260 265 270	
gtc att aaa ctt tat atc ccg gaa ccc ctt tat atg act gaa gaa gaa	864
Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu	
275 280 285	
tcg tct gga atc act cag gat ggt gaa gct ata cca aga ctt gca ggg	912
Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly	
290 295 300	
aca aga ctc gca gca tcg tat gtg aat ttc tac atc gcc aat gga gga	960
Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly	
305 310 315 320	
ata atc gct cca caa ttc ggt gat cca ata cgt gat aaa gaa gcg att	1008
Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile	
325 330 335	
cgt gtc ctc tcg gat aca ttt cct cat cac tcg gtt gtg gga atc gag	1056

Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu  
 340 345 350  
 aat gca aga gag atc gtt ctt gct gga gga aac att cat tgt ata acg 1104  
 Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr  
 355 360 365  
 cag cag cag ccg gcg gag cct act tcc gtc gcc gaa aat ggc cac tga 1152  
 Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His  
 370 375 380  
  
 <210> 66  
 <211> 383  
 <212> PRT  
 <213> Arabidopsis thaliana  
  
 <400> 66  
 Met Glu Glu Ser Arg Glu Ser Pro Ala Glu His Gly Tyr Tyr Met Pro  
 1 5 10 15  
 Ala Glu Trp Asp Ser His Ala Gln Thr Trp Ile Gly Trp Pro Glu Arg  
 20 25 30  
 Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala  
 35 40 45  
 Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala  
 50 55 60  
 Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile  
 65 70 75 80  
 Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly  
 85 90 95  
 Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn  
 100 105 110  
 Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala  
 115 120 125  
 Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg  
 130 135 140

Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile  
 145 150 155 160

Leu Glu Gly Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val  
 165 170 175

Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys  
 180 185 190

Glu Gln Ile Glu Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe  
 195 200 205

Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His  
 210 215 220

Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser  
 225 230 235 240

Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala  
 245 250 255

Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln  
 260 265 270

Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu  
 275 280 285

Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly  
 290 295 300

Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly  
 305 310 315 320

Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile  
 325 330 335

Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu  
 340 345 350

Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr  
 355 360 365

Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His  
 370 375 380

&lt;210&gt; 67

&lt;211&gt; 1935

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1935)

&lt;223&gt; 46250

&lt;400&gt; 67

atg gct agt ctt ctt cga tcc tta atc ctt ttg cta atc gtg caa tca	48
Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Leu Ile Val Gln Ser	
1 5 10 15	
ttt ttg gtt gcg atc gct ttc ggg tcg aaa gaa gtt gaa gaa ttc agc	96
Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser	
20 25 30	
gag gca ttg ctc ttg aag cct tta cct gat cga aaa gtt tta gct cac	144
Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His	
35 40 45	
ttc cac ttc gag aac cga gct cct ccg tca aac tcc cat ggc cgc cat	192
Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His	
50 55 60	
cac cat ctc ttc ccg aaa gct att tct cag ttg gtt cag aag ttt cgg	240
His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg	
65 70 75 80	
gtc aag gag atg gag tta tct ttt act cag ggt cga tgg aac cat gaa	288
Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu	
85 90 95	
cat tgg gga gga ttt gac cct cta tca agt atg aat gcg aag cct gtt	336
His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val	
100 105 110	
ggg gtg gag ctg tgg gct gtg ttt gat gtt cct cag tct cag gtt gat	384
Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp	
115 120 125	
act tct tgg aag aac tta act cat gca ctg tca ggg ctt ttc tgt gct	432
Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala	
130 135 140	
tcc atc aat ttt cta gaa tct tcc act tca tat gct gct cct aca tgg	480
Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp	
145 150 155 160	



gga ttt gga ccc aat tct gac aag ctg agg tat ggt tca ctg cca cgt Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg 165 170 175	528
gaa gct gtt tgt act gag aac ttg acc cca tgg cta aag tta ctt cct Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro 180 185 190	576
tgt aga gat aag gat ggt att tct gcg tta atg aat agg cca tct gtt Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val 195 200 205	624
tac aga ggg ttt tat cat tct cag aga ttg cat tta tcc acg gtt gaa Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu 210 215 220	672
tct ggt caa gag gga ttg ggt tct ggt ata gtg ctg gag cag acg ctt Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu 225 230 235 240	720
act gtt gtt ctt cag cct gag act act tct gtt gaa tca aat atg cag Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln 245 250 255	768
cca agt tgg tcc ctc agc tcc ctc ttt ggg aga caa gtt gtt ggg aga Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg 260 265 270	816
tgt gtt ctt gca aag tca agt aat gtg tat ctt caa ttg gaa ggt ctt Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu 275 280 285	864
ctt ggt tac gaa tca aaa aac gtg gat aca gaa ata gaa gca cac caa Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln 290 295 300	912
cta tgg aag aat gca gag ttt gaa ttg tct ctt aag cca gag agg gtt Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val 305 310 315 320	960
att cga gaa agc tgc agc ttt ctt ttt att ttt gat att gac aaa tca Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser 325 330 335	1008
agt gac agc gag cca ttt gat ctt ggc ctt act tgg aag cgt ccc tca Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser 340 345 350	1056
aag tgg tca tgt caa caa gct cca tta cac tcg agt cgg ttt ttg atg Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met 355 360 365	1104
gga agc ggg aac gaa aga ggt gca ata gcc atc ttg tta aaa gcg aca Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr 370 375 380	1152
gaa tct cag gag aag tta tca ggc aga gat ctc act aat ggc caa tgt Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys 385 390 395 400	1200

aca ata aaa gca aat atc ttc cag att ttc cca tgg tat att aag gtt	1248
Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val	
405 410 415	
tat tat cat act cta caa atc ttt gtg gat caa caa cag aag aca gac	1296
Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp	
420 425 430	
agt gag gtc tta aag aag atc aat gtc tca cca tct acg gat aag gtg	1344
Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val	
435 440 445	
tca tct ggc atg atg gag atg atg ttg gaa cta cca tgt gaa gtg aaa	1392
Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys	
450 455 460	
tct gta gcc ata tca att gaa tat gat aag ggt ttt ctg cat ata gat	1440
Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp	
465 470 475 480	
gaa tat cct cct gat gct aat caa gga ttc gac att cca tcg gct ttg	1488
Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu	
485 490 495	
ata agc ttc ccc gat cat cat gct agt tta gat ttc caa gaa gag ctc	1536
Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu	
500 505 510	
agc aac tcg ccc tta tta tca agt tta aag gaa aaa tcc tta gta cgc	1584
Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg	
515 520 525	
tct tac aca gaa gta ttg ctc gta cct ttg aca acc cct gat ttt agc	1632
Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser	
530 535 540	
atg cct tac aac gta atc acg atc aca tgc acc atc ttc gca ttg tat	1680
Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr	
545 550 555 560	
ttt gga tca ttg cta aat gtt cta cgt aga cga att ggt gaa gaa gaa	1728
Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu	
565 570 575	
agg ttt ctc aaa agc caa gca gga aag aaa aca ggt ggg ctt aag cag	1776
Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln	
580 585 590	
tta tta tcg aga atc aca gcc aag att aga ggg aga cca att gaa gca	1824
Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala	
595 600 605	
cca tca tca tca gaa gct gaa tct tcg gtc ttg tct agt aaa ctt atc	1872
Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile	
610 615 620	
tta aaa atc ata tta gtt gca gga gct gct gca gcg tgg caa tat ttt	1920
Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Ala Trp Gln Tyr Phe	
625 630 635 640	

tcc acg gac gag tag  
Ser Thr Asp Glu

1935

&lt;210&gt; 68

&lt;211&gt; 644

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 68

Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Leu Ile Val Gln Ser  
1 5 10 15

Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser  
20 25 30

Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His  
35 40 45

Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His  
50 55 60

His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg  
65 70 75 80

Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu  
85 90 95

His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val  
100 105 110

Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp  
115 120 125

Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala  
130 135 140

Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp  
145 150 155 160

Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg  
165 170 175

155

Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro  
 180 185 190

Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val  
 195 200 205

Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu  
 210 215 220

Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu  
 225 230 235 240

Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln  
 245 250 255

Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg  
 260 265 270

Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu  
 275 280 285

Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln  
 290 295 300

Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val  
 305 310 315 320

Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser  
 325 330 335

Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser  
 340 345 350

Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met  
 355 360 365

Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr  
 370 375 380

Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys  
 385 390 395 400

Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val  
 405 410 415

Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp  
 420 425 430

Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val  
 435 440 445

Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys  
 450 455 460

Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp  
 465 470 475 480

Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu  
 485 490 495

Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu  
 500 505 510

Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg  
 515 520 525

Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser  
 530 535 540

Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr  
 545 550 555 560

Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu  
 565 570 575

Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln  
 580 585 590

Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala  
 595 600 605

Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile  
 610 615 620

Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Trp Gln Tyr Phe  
 625 630 635 640

Ser Thr Asp Glu

&lt;210&gt; 69

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(210)

&lt;223&gt; 47050A

&lt;400&gt; 69

atg ggt gga gga gga cat ggc gga ggt ata act tac aag gga gtc act	48
Met Gly Gly Gly Gly His Gly Gly Gly Ile Thr Tyr Lys Gly Val Thr	
1 5 10 15	

gtc cac act ccc aag act tgg cac acc gtc acc gga aaa ggc ttg tgc	96
Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys	
20 25 30	

gcc gtt atg tgg ttc tgg att ctg tac agg gca aag caa gat ggt cct	144
Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro	
35 40 45	

gta gtt atg gga tgg agg cac cct tgg gat ggt cat ggt gat cac ggt	192
Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly	
50 55 60	

cac gga gat cat cac tag	210
His Gly Asp His His	
65	

&lt;210&gt; 70

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 70

Met Gly Gly Gly Gly His Gly Gly Gly Ile Thr Tyr Lys Gly Val Thr
1 5 10 15

Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys  
 20 25 30

Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro  
 35 40 45

Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly  
 50 55 60

His Gly Asp His His  
 65

<210> 71

<211> 978

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(978)

<223> 52949A

<400> 71  
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 Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro  
 1 5 10 15  
 act aac ctt cgt tca aat cac cat ctc ccc act ttc ttc ccc aag aat 96  
 Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn  
 20 25 30  
 tat ctc att tgc tct cat tcc act tct tct cgc ttc gaa tcg ctc tcg 144  
 Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser  
 35 40 45  
 gtt tca tcg atc gga act gga tct acc aag aaa tca tcc gat act cgg 192  
 Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg  
 50 55 60  
 aga aag gta aag agc atg gct acg aca aat ata gga aag gag gag aag 240  
 Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys  
 65 70 75 80  
 aaa aga gtc gag att tat gat ctc gaa gag aat tta gtg att gat ttg 288  
 Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu  
 85 90 95

gct aaa ttc aca gca gat ctc tcc gat aag ttt tgt aaa gag aga ggc 336  
 Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly  
 100 105 110

gct ttc acc gtc gtt gtc tcc ggt ggc tct ctc atc aaa tca ctc cgg 384  
 Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg  
 115 120 125

aaa tta gta gaa tct cct tac gtt gat tct ata gat tgg gca agg tgg 432  
 Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp  
 130 135 140

cat ttt ttc tgg gtt gac gag aga gtt gtt ccc aag aat cac gat gat 480  
 His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp  
 145 150 155 160

agc aac tat aaa ctc gct tat gat agt ttt cta tcc aag gta cca att 528  
 Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile  
 165 170 175

ccg cct gga aat gta tat gca atc aac gaa gcc ctc tcc gct gag gct 576  
 Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala  
 180 185 190

gca gcg gat gat tac gag acc tgc ctc aaa cat ttg gtc aac acc aac 624  
 Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn  
 195 200 205

att ctc cgt gta tct gaa tca act ggc ttt ccc aaa ttt gat ctc atg 672  
 Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met  
 210 215 220

ctt cta ggt atg gga cct gat ggt cat gtg gca tca tta ttc cct ggg 720  
 Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly  
 225 230 235 240

cat ggt ctc tgc aac gag agc aag aaa tgg gta gtt tca atc tct gac 768  
 His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp  
 245 250 255

tct cca aaa cca ccg tct gag aga atc acc ttc acg ttc ccg gtc atc 816  
 Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile  
 260 265 270

aac tca tct gca cat gta gct cta gtt gtt tgc ggt tct ggg aaa gct 864  
 Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala  
 275 280 285

gaa gct gtg gag gca gct tta aag aag act ggg aat gta cca cct gct 912  
 Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala  
 290 295 300

ggt tct gtt tct gct gaa gac gag ttg gtt tgg ttc ctg gac aaa cca 960  
 Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro  
 305 310 315 320

gca tct tcc aag ctc taa 978  
 Ala Ser Ser Lys Leu  
 325



&lt;210&gt; 72

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 72

Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro  
 1 5 10 15

Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn  
 20 25 30

Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser  
 35 40 45

Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg  
 50 55 60

Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys  
 65 70 75 80

Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu  
 85 90 95

Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly  
 100 105 110

Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg  
 115 120 125

Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp  
 130 135 140

His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp  
 145 150 155 160

Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile  
 165 170 175

Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala  
 180 185 190

Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn  
 195 200 205

Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met  
 210 215 220

Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly  
 225 230 235 240

His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp  
 245 250 255

Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile  
 260 265 270

Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala  
 275 280 285

Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala  
 290 295 300

Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro  
 305 310 315 320

Ala Ser Ser Lys Leu  
 325

<210> 73

<211> 2343

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (2343)

<223> 53210A

<400> 73

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48

Met Ala Pro Ala Leu Ser Arg Ser Leu Tyr Thr Ser Pro Leu Thr Ser	
1 5 10 15	
ggt cca atc act cct gtc tct tct cgt ctc tct cat ctg aga agc tcg	96
Val Pro Ile Thr Pro Val Ser Ser Arg Leu Ser His Leu Arg Ser Ser	
20 25 30	
ttt ctc cca cac ggc ggc gct tta aga acc ggc gtt tcg tgt agc tgg	144
Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp	
35 40 45	
aat ctc gaa aag aga tgt aac cga ttc gcc gtg aag tgt gac gcc gcc	192
Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala	
50 55 60	
gtg gcg gag aaa gag acc act gaa gaa ggg tca ggt gag aag ttt gag	240
Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu	
65 70 75 80	
tac caa gct gag gtt agt aga ttg ttg gat ttg att gtt cat agc tta	288
Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu	
85 90 95	
tac agt cac aag gag gtg ttt ctc agg gag ctt gta agt aat gca agt	336
Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser	
100 105 110	
gat gct ttg gat aag ctg agg ttc ttg agt gta aca gag cct tct ttg	384
Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu	
115 120 125	
ctt gga gat ggt gga gat ctt gag att agg att aag cct gat cct gat	432
Leu Gly Asp Gly Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp	
130 135 140	
aac ggc acc atc acc ata act gat act ggt att gga atg aca aag gaa	480
Asn Gly Thr Ile Thr Ile Thr Asp Thr Gly Ile Gly Met Thr Lys Glu	
145 150 155 160	
gaa ctt att gat tgc ctt gga act att gct caa agt ggt act tcg aaa	528
Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys	
165 170 175	
ttc ttg aag gct cta aag gaa aac aag gac ctt ggt gct gac aac ggt	576
Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly	
180 185 190	
ttg atc gga cag ttt ggt gtt ggg ttt tac tct gct ttc tta gtt gct	624
Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala	
195 200 205	
gag aag gtt gtt gtg tcc acc aaa agc ccc aaa tct gac aag caa tat	672
Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr	
210 215 220	
ggt tgg gaa tcg gtt gcc gat agt agc tcg tat ctg atc aga gaa gaa	720
Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu	
225 230 235 240	
aca gac cct gat aac att cta cgt cgt gga aca caa atc acc ttg tat	768

Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr	
245	250 255
ctg agg gag gat gat aaa tac gaa ttt gcg gag tct aca agg atc aag	816
Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys	
260	265 270
aac ctc gtg aag aat tac tct cag ttc gtt ggg ttt cct atc tat aca	864
Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr	
275	280 285
tgg cag gag aaa tca agg act ata gag gtc gaa gag gac gaa cca gtt	912
Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Glu Asp Glu Pro Val	
290	295 300
aag gaa gga gaa gag ggt gag cca aag aaa aag aag acc act aaa act	960
Lys Glu Gly Glu Glu Gly Glu Pro Lys Lys Lys Lys Thr Thr Lys Thr	
305	310 315 320
gag aag tat tgg gat tgg gaa cta gcc aac gag acc aaa ccg cta tgg	1008
Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp	
325	330 335
atg cgc aat tcg aag gaa gtg gaa aaa gga gag tac aat gag ttc tac	1056
Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr	
340	345 350
aaa aag gct ttc aat gag ttc ttg gat cca ctt gct cac aca cac ttc	1104
Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe	
355	360 365
aca act gag ggt gag gtt gag ttc agg agc att ttg tac atc cct ggg	1152
Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly	
370	375 380
atg ggt cct ctt aac aat gaa gat gtt aca aac ccg aaa aca aag aac	1200
Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn	
385	390 395 400
att cgt ctc tac gtg aag cgt gtg ttt atc tct gac gat ttt gat gga	1248
Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly	
405	410 415
gag ctt ttc ccg aga tat ctg agc ttt gtg aag gga gtt gtg gac tct	1296
Glu Leu Phe Pro Arg Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser	
420	425 430
gat gat ctt cct ctt aat gtt tct cgt gaa att ctc caa gaa agc aga	1344
Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg	
435	440 445
att gta aga atc atg aga aag agg ctc att aga aaa acc ttt gac atg	1392
Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met	
450	455 460
ata caa gaa atc tct gag agt gaa aac aaa gag gat tac aag aaa ttc	1440
Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe	
465	470 475 480
tgg gag aac ttt ggt aga ttc ctt aaa ttg ggt tgt att gaa gac acc	1488

Trp	Glu	Asn	Phe	Gly	Arg	Phe	Leu	Lys	Leu	Gly	Cys	Ile	Glu	Asp	Thr		
				485					490					495			
ggt	aac	cac	aag	cgt	atc	aca	ccg	cta	ctt	aga	ttc	ttc	agt	tcc	aag		1536
Gly	Asn	His	Lys	Arg	Ile	Thr	Pro	Leu	Leu	Arg	Phe	Phe	Ser	Ser	Lys		
			500					505					510				
aat	gaa	gag	gaa	ttg	aca	agc	ttg	gat	gat	tat	atc	gag	aac	atg	gga		1584
Asn	Glu	Glu	Glu	Leu	Thr	Ser	Leu	Asp	Asp	Tyr	Ile	Glu	Asn	Met	Gly		
			515				520					525					
gag	aac	caa	aag	gcg	atc	tac	tac	ctc	gca	act	gat	agt	ctt	aaa	agt		1632
Glu	Asn	Gln	Lys	Ala	Ile	Tyr	Tyr	Leu	Ala	Thr	Asp	Ser	Leu	Lys	Ser		
	530					535					540						
gcc	aag	tct	gcc	cct	ttc	ttg	gag	aaa	cta	atc	caa	aaa	gat	atc	gag		1680
Ala	Lys	Ser	Ala	Pro	Phe	Leu	Glu	Lys	Leu	Ile	Gln	Lys	Asp	Ile	Glu		
	545				550					555					560		
ggt	cta	tat	ttg	ggt	gaa	cca	atc	gat	gaa	ggt	gct	att	cag	aat	ttg		1728
Val	Leu	Tyr	Leu	Val	Glu	Pro	Ile	Asp	Glu	Val	Ala	Ile	Gln	Asn	Leu		
			565					570						575			
caa	acc	tac	aaa	gaa	aag	aaa	ttc	ggt	gat	atc	agt	aaa	gaa	gat	ttg		1776
Gln	Thr	Tyr	Lys	Glu	Lys	Lys	Phe	Val	Asp	Ile	Ser	Lys	Glu	Asp	Leu		
			580				585						590				
gaa	ctc	gga	gat	gaa	gat	gaa	gta	aag	gac	agg	gaa	gcg	aaa	caa	gag		1824
Glu	Leu	Gly	Asp	Glu	Asp	Glu	Val	Lys	Asp	Arg	Glu	Ala	Lys	Gln	Glu		
		595					600					605					
ttt	aac	ctt	ctc	tgt	gac	tgg	ata	aaa	cag	cag	ctc	ggt	gac	aaa	gtt		1872
Phe	Asn	Leu	Leu	Cys	Asp	Trp	Ile	Lys	Gln	Gln	Leu	Gly	Asp	Lys	Val		
	610					615					620						
gca	aaa	gtc	caa	gtc	tca	aac	cgt	ttg	agc	tct	tct	cct	tgt	gtg	ctt		1920
Ala	Lys	Val	Gln	Val	Ser	Asn	Arg	Leu	Ser	Ser	Ser	Pro	Cys	Val	Leu		
	625					630				635					640		
gtc	tct	ggc	aaa	ttc	ggg	tgg	tca	gct	aat	atg	gaa	agg	cta	atg	aag		1968
Val	Ser	Gly	Lys	Phe	Gly	Trp	Ser	Ala	Asn	Met	Glu	Arg	Leu	Met	Lys		
			645					650					655				
gca	cag	gct	ctt	gga	gac	act	tca	agc	ctg	gag	ttc	atg	aga	ggt	agg		2016
Ala	Gln	Ala	Leu	Gly	Asp	Thr	Ser	Ser	Leu	Glu	Phe	Met	Arg	Gly	Arg		
			660					665					670				
aga	ata	cta	gag	atc	aat	cca	gat	cat	ccc	atc	atc	aaa	gac	ttg	aac		2064
Arg	Ile	Leu	Glu	Ile	Asn	Pro	Asp	His	Pro	Ile	Ile	Lys	Asp	Leu	Asn		
		675				680						685					
gct	gct	tgt	aag	aat	gca	cca	gag	agc	act	gaa	gca	aca	aga	gtg	gtc		2112
Ala	Ala	Cys	Lys	Asn	Ala	Pro	Glu	Ser	Thr	Glu	Ala	Thr	Arg	Val	Val		
		690				695					700						
gat	ctc	ttg	tat	gac	act	gct	ata	ata	tca	agt	gga	ttc	act	cct	gat		2160
Asp	Leu	Leu	Tyr	Asp	Thr	Ala	Ile	Ile	Ser	Ser	Gly	Phe	Thr	Pro	Asp		
	705				710				715						720		
agc	ccg	gcc	gag	ctc	ggg	aac	aag	ata	tat	gag	atg	atg	gca	atg	gcg		2208

Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala  
 725 730 735

gtt gga gga aga tgg ggc aga gtt gaa gaa gaa gaa gaa agc tcg act 2256  
 Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Glu Ser Ser Thr  
 740 745 750

gtg aat gaa gga gat gac aaa agc gga gaa aca gag gta gtt gaa cca 2304  
 Val Asn Glu Gly Asp Asp Lys Ser Gly Glu Thr Glu Val Val Glu Pro  
 755 760 765

tct gaa gtg agg gca gag agt gat cct tgg caa gat tga 2343  
 Ser Glu Val Arg Ala Glu Ser Asp Pro Trp Gln Asp  
 770 775 780

&lt;210&gt; 74

&lt;211&gt; 780

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 74

Met Ala Pro Ala Leu Ser Arg Ser Leu Tyr Thr Ser Pro Leu Thr Ser  
 1 5 10 15

Val Pro Ile Thr Pro Val Ser Ser Arg Leu Ser His Leu Arg Ser Ser  
 20 25 30

Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp  
 35 40 45

Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala  
 50 55 60

Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu  
 65 70 75 80

Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu  
 85 90 95

Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser  
 100 105 110

Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu  
 115 120 125

Leu Gly Asp Gly Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp  
 130 135 140

Asn Gly Thr Ile Thr Ile Thr Asp Thr Gly Ile Gly Met Thr Lys Glu  
 145 150 155 160

Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys  
 165 170 175

Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly  
 180 185 190

Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala  
 195 200 205

Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr  
 210 215 220

Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu  
 225 230 235 240

Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr  
 245 250 255

Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys  
 260 265 270

Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr  
 275 280 285

Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Glu Asp Glu Pro Val  
 290 295 300

Lys Glu Gly Glu Glu Gly Glu Pro Lys Lys Lys Lys Thr Thr Lys Thr  
 305 310 315 320

Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp  
 325 330 335

Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr  
 340 345 350

Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe  
 355 360 365

Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly  
 370 375 380

Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn  
 385 390 395 400

Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly  
 405 410 415

Glu Leu Phe Pro Arg Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser  
 420 425 430

Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg  
 435 440 445

Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met  
 450 455 460

Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe  
 465 470 475 480

Trp Glu Asn Phe Gly Arg Phe Leu Lys Leu Gly Cys Ile Glu Asp Thr  
 485 490 495

Gly Asn His Lys Arg Ile Thr Pro Leu Leu Arg Phe Phe Ser Ser Lys  
 500 505 510

Asn Glu Glu Glu Leu Thr Ser Leu Asp Asp Tyr Ile Glu Asn Met Gly  
 515 520 525

Glu Asn Gln Lys Ala Ile Tyr Tyr Leu Ala Thr Asp Ser Leu Lys Ser  
 530 535 540

Ala Lys Ser Ala Pro Phe Leu Glu Lys Leu Ile Gln Lys Asp Ile Glu  
 545 550 555 560

Val Leu Tyr Leu Val Glu Pro Ile Asp Glu Val Ala Ile Gln Asn Leu  
 565 570 575

Gln Thr Tyr Lys Glu Lys Lys Phe Val Asp Ile Ser Lys Glu Asp Leu  
 580 585 590

Glu Leu Gly Asp Glu Asp Glu Val Lys Asp Arg Glu Ala Lys Gln Glu  
 595 600 605



Phe Asn Leu Leu Cys Asp Trp Ile Lys Gln Gln Leu Gly Asp Lys Val  
 610 615 620

Ala Lys Val Gln Val Ser Asn Arg Leu Ser Ser Ser Pro Cys Val Leu  
 625 630 635 640

Val Ser Gly Lys Phe Gly Trp Ser Ala Asn Met Glu Arg Leu Met Lys  
 645 650 655

Ala Gln Ala Leu Gly Asp Thr Ser Ser Leu Glu Phe Met Arg Gly Arg  
 660 665 670

Arg Ile Leu Glu Ile Asn Pro Asp His Pro Ile Ile Lys Asp Leu Asn  
 675 680 685

Ala Ala Cys Lys Asn Ala Pro Glu Ser Thr Glu Ala Thr Arg Val Val  
 690 695 700

Asp Leu Leu Tyr Asp Thr Ala Ile Ile Ser Ser Gly Phe Thr Pro Asp  
 705 710 715 720

Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala  
 725 730 735

Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Glu Ser Ser Thr  
 740 745 750

Val Asn Glu Gly Asp Asp Lys Ser Gly Glu Thr Glu Val Val Glu Pro  
 755 760 765

Ser Glu Val Arg Ala Glu Ser Asp Pro Trp Gln Asp  
 770 775 780

<210> 75

<211> 2760

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (2760)

&lt;223&gt; 55483

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 Met Asn Met Asn Phe Ser Phe Cys Ser Thr Ser Ser Glu Leu Ser Tyr  
 1 5 10 15

cca agt gag aat gtt ctg aga ttt tct gtt gca agt cgg ctg ttt tct 96  
 Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser  
 20 25 30

cct aaa tgg aag aaa agt ttc att agt tta cct tgt cgt agt aaa act 144  
 Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr  
 35 40 45

acg agg aag gtt ttg gcg tca agc cgt tat gtg cca ggg aaa ttg gaa 192  
 Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu  
 50 55 60

gat ttg tcg gtt gtt aag aag agt tta ccg aga aga gaa cct gtg gag 240  
 Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu  
 65 70 75 80

aag ctt ggt ttt gtg agg act ttg ttg att gat aat tat gat agt tat 288  
 Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr  
 85 90 95

aca ttc aat ata tat cag gct ctg agt act att aat gga gtg cct cct 336  
 Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro  
 100 105 110

gtc gtt att cgg aat gat gag tgg acg tgg gaa gaa gct tac cat tac 384  
 Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr  
 115 120 125

tta tat gaa gat gtt gct ttt gat aat att gtt ata tcg cct gga cct 432  
 Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro  
 130 135 140

ggg tcg cct atg tgt cca gct gat ata gga ata tgt ctt cgt ctt ttg 480  
 Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu  
 145 150 155 160

ctt gaa tgc cgt gat atc cca att cta ggc gtc tgc ctt ggc cac cag 528  
 Leu Glu Cys Arg Asp Ile Pro Ile Leu Gly Val Cys Leu Gly His Gln  
 165 170 175

gca cta ggt tat gtc cat gga gct cat gtg gtg cat gcc ccg gaa cca 576  
 Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro  
 180 185 190

gtc cat gga cgg ttg agt ggg att gaa cat gat ggg aac ata ttg ttt 624  
 Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe  
 195 200 205

tct gat att cca tcc ggg aga aac tct gat ttt aag gtt gtt aga tac 672  
 Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr  
 210 215 220

cat tca ctg atc ata gat aag gaa tca cta cca aag gaa ctt gta cca His Ser Leu Ile Ile Asp Lys Glu Ser Leu Pro Lys Glu Leu Val Pro 225 230 235 240	720
ata gcg tgg acg att tat gat gac act ggc tct ttc tct gag aag aat Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn 245 250 255	768
tcc tgt gtt cct gtg aat aac act ggg agc cca ctt ggg aac gga tct Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser 260 265 270	816
gtc att cct gtt tca gaa aag tta gaa aat cga agt cat tgg cct tcg Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser 275 280 285	864
tcc cat gtt aat ggg aaa caa gat aga cac att ctc atg ggc atc atg Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met 290 295 300	912
cat tct tct ttt ccc cat tat ggt tta cag ttt cat cca gaa agt att His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile 305 310 315 320	960
gct act acc tat ggt agt cag tta ttt aaa aat ttc aag gac ata act Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr 325 330 335	1008
gtg aat tat tgg agt cgg tgc aaa tct aca tcc ctg cgt cga aga aac Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Asn 340 345 350	1056
ata aat gac act gca aac atg cag gtg cct gat gct act caa ttg ctg Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu 355 360 365	1104
aaa gaa ctt tct aga act aga tgt aca gga aat ggt tct agc tat ttt Lys Glu Leu Ser Arg Thr Arg Cys Thr Gly Asn Gly Ser Ser Tyr Phe 370 375 380	1152
ggg aac cct aag tct ctg ttt tct gcc aag aca aat ggt gta gac gtc Gly Asn Pro Lys Ser Leu Phe Ser Ala Lys Thr Asn Gly Val Asp Val 385 390 395 400	1200
ttt gat atg gtg gat tca tca tat cca aaa cca cat aca aaa ttg ctg Phe Asp Met Val Asp Ser Ser Tyr Pro Lys Pro His Thr Lys Leu Leu 405 410 415	1248
agg ttg aaa tgg aag aag cat gaa cgt ctt gcg cat aaa gtt ggt gga Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly 420 425 430	1296
gta aga aat ata ttt atg gaa ctc ttt ggc aag aat aga gga aat gat Val Arg Asn Ile Phe Met Glu Leu Phe Gly Lys Asn Arg Gly Asn Asp 435 440 445	1344
act ttt tgg ctg gat act tct tct agt gac aag gct aga gga cga ttt Thr Phe Trp Leu Asp Thr Ser Ser Ser Asp Lys Ala Arg Gly Arg Phe 450 455 460	1392

tct ttc atg ggc ggt aaa ggt gga tct ctc tgg aag caa ttg aca ttt Ser Phe Met Gly Gly Lys Gly Gly Ser Leu Trp Lys Gln Leu Thr Phe 465 470 475 480	1440
agt tta tct gat caa agt gag gtt aca tca aaa cat gcg gga cat ctt Ser Leu Ser Asp Gln Ser Glu Val Thr Ser Lys His Ala Gly His Leu 485 490 495	1488
ctg att gaa gat tct cag agt tct act gag aaa caa ttc ttg gaa gaa Leu Ile Glu Asp Ser Gln Ser Ser Thr Glu Lys Gln Phe Leu Glu Glu 500 505 510	1536
ggc ttt ctt gat ttt ctc cgt aag gag ctt tca tct atc tct tat gat Gly Phe Leu Asp Phe Leu Arg Lys Glu Leu Ser Ser Ile Ser Tyr Asp 515 520 525	1584
gag aag gac ttc gaa gag ttg cct ttt gat ttt tgc ggt gga tac gta Glu Lys Asp Phe Glu Glu Leu Pro Phe Asp Phe Cys Gly Gly Tyr Val 530 535 540	1632
ggt tgt att ggg tat gat att aaa gtg gaa tgt gga atg cca att aat Gly Cys Ile Gly Tyr Asp Ile Lys Val Glu Cys Gly Met Pro Ile Asn 545 550 555 560	1680
cgt cac aaa tcc aac gct cca gat gca tgt ttc ttc ttt gcg gat aat Arg His Lys Ser Asn Ala Pro Asp Ala Cys Phe Phe Phe Ala Asp Asn 565 570 575	1728
gtt gtc gcc att gat cat caa ctc gat gac gtt tat ata tta tcg ctt Val Val Ala Ile Asp His Gln Leu Asp Asp Val Tyr Ile Leu Ser Leu 580 585 590	1776
tac gaa gag gga act gca gaa acc tct ttc ctg aat gat act gaa gag Tyr Glu Glu Gly Thr Ala Glu Thr Ser Phe Leu Asn Asp Thr Glu Glu 595 600 605	1824
aag ctc att agc ttg atg ggt ttg tcc aca aga aag ttg gag gat caa Lys Leu Ile Ser Leu Met Gly Leu Ser Thr Arg Lys Leu Glu Asp Gln 610 615 620	1872
act ctt cca gtt ata gat tca tct caa tcc aaa aca agt ttt gtt cct Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro 625 630 635 640	1920
gac aaa tcc cga gag cag tat atc aac gat gtt cag agc tgt atg aag Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys 645 650 655	1968
tat atc aaa gac ggg gag agc tac gag ctt tgt ctc act act caa aac Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn 660 665 670	2016
aga agg aaa ata gga aat gct gat cct ttg gga ctt tat ctc cac ctg Arg Arg Lys Ile Gly Asn Ala Asp Pro Leu Gly Leu Tyr Leu His Leu 675 680 685	2064
aga gag agg aat cca gca cca tat gca gca ttt ctc aac ttc tca aat Arg Glu Arg Asn Pro Ala Pro Tyr Ala Ala Phe Leu Asn Phe Ser Asn 690 695 700	2112

gca aat ctg tct tta tgc tct tcg tcc cct gaa agg ttt ctt aag ctg 2160  
 Ala Asn Leu Ser Leu Cys Ser Ser Ser Pro Glu Arg Phe Leu Lys Leu  
 705 710 715 720

gac aga aat gga atg ctt gaa gca aag ccg att aag ggt act ata gct 2208  
 Asp Arg Asn Gly Met Leu Glu Ala Lys Pro Ile Lys Gly Thr Ile Ala  
 725 730 735

cgt ggc tcc acg cct gaa gaa gat gaa ttt ctt aaa ttg caa ttg aaa 2256  
 Arg Gly Ser Thr Pro Glu Glu Asp Glu Phe Leu Lys Leu Gln Leu Lys  
 740 745 750

ctc agt gag aag aat caa gcc gag aat ctg atg att gtt gac ctt cta 2304  
 Leu Ser Glu Lys Asn Gln Ala Glu Asn Leu Met Ile Val Asp Leu Leu  
 755 760 765

agg aat gat ctc ggt cgt gtc tgt gag cct ggc tca gtc cat gta cct 2352  
 Arg Asn Asp Leu Gly Arg Val Cys Glu Pro Gly Ser Val His Val Pro  
 770 775 780

aac ctc atg gat gta gaa tca tac aca aca gta cat aca atg gtg agc 2400  
 Asn Leu Met Asp Val Glu Ser Tyr Thr Thr Val His Thr Met Val Ser  
 785 790 795 800

acg atc cgt gga ctg aaa aaa aca gat att agt cca gtg gaa tgt gta 2448  
 Thr Ile Arg Gly Leu Lys Lys Thr Asp Ile Ser Pro Val Glu Cys Val  
 805 810 815

aga gct gct ttc cct ggc ggt tca atg act ggt gcc cca aaa cta aga 2496  
 Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly Ala Pro Lys Leu Arg  
 820 825 830

tct gtt gag att ctc gat tct cta gag aac tgt tcg aga ggc ctt tac 2544  
 Ser Val Glu Ile Leu Asp Ser Leu Glu Asn Cys Ser Arg Gly Leu Tyr  
 835 840 845

tct ggc tca atc ggg tat ttc tcg tat aat ggt acg ttt gat ctg aat 2592  
 Ser Gly Ser Ile Gly Tyr Phe Ser Tyr Asn Gly Thr Phe Asp Leu Asn  
 850 855 860

att gtg ata aga aca gta ata ata cat gaa gat gaa gct tcc att gga 2640  
 Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly  
 865 870 875 880

gca gga gga gct att gtt gca tta tca agt cca gaa gat gag ttt gag 2688  
 Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu  
 885 890 895

gaa atg att ctt aag act aga gct cct gct aat gca gtc atg gag ttt 2736  
 Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe  
 900 905 910

tgt agt gat cag agg aga caa tag 2760  
 Cys Ser Asp Gln Arg Arg Gln  
 915

&lt;210&gt; 76

&lt;211&gt; 919

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

Met Asn Met Asn Phe Ser Phe Cys Ser Thr Ser Ser Glu Leu Ser Tyr  
 1 5 10 15

Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser  
 20 25 30

Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr  
 35 40 45

Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu  
 50 55 60

Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu  
 65 70 75 80

Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr  
 85 90 95

Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro  
 100 105 110

Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr  
 115 120 125

Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro  
 130 135 140

Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu  
 145 150 155 160

Leu Glu Cys Arg Asp Ile Pro Ile Leu Gly Val Cys Leu Gly His Gln  
 165 170 175

Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro  
 180 185 190

Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe  
 195 200 205

Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr  
 210 215 220

His Ser Leu Ile Ile Asp Lys Glu Ser Leu Pro Lys Glu Leu Val Pro  
 225 230 235 240

Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn  
 245 250 255

Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser  
 260 265 270

Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser  
 275 280 285

Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met  
 290 295 300

His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile  
 305 310 315 320

Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr  
 325 330 335

Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Arg Asn  
 340 345 350

Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu  
 355 360 365

Lys Glu Leu Ser Arg Thr Arg Cys Thr Gly Asn Gly Ser Ser Tyr Phe  
 370 375 380

Gly Asn Pro Lys Ser Leu Phe Ser Ala Lys Thr Asn Gly Val Asp Val  
 385 390 395 400

Phe Asp Met Val Asp Ser Ser Tyr Pro Lys Pro His Thr Lys Leu Leu  
 405 410 415

Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly  
 420 425 430

Val Arg Asn Ile Phe Met Glu Leu Phe Gly Lys Asn Arg Gly Asn Asp  
 435 440 445

Thr Phe Trp Leu Asp Thr Ser Ser Ser Asp Lys Ala Arg Gly Arg Phe  
 450 455 460

Ser Phe Met Gly Gly Lys Gly Gly Ser Leu Trp Lys Gln Leu Thr Phe  
 465 470 475 480

Ser Leu Ser Asp Gln Ser Glu Val Thr Ser Lys His Ala Gly His Leu  
 485 490 495

Leu Ile Glu Asp Ser Gln Ser Ser Thr Glu Lys Gln Phe Leu Glu Glu  
 500 505 510

Gly Phe Leu Asp Phe Leu Arg Lys Glu Leu Ser Ser Ile Ser Tyr Asp  
 515 520 525

Glu Lys Asp Phe Glu Glu Leu Pro Phe Asp Phe Cys Gly Gly Tyr Val  
 530 535 540

Gly Cys Ile Gly Tyr Asp Ile Lys Val Glu Cys Gly Met Pro Ile Asn  
 545 550 555 560

Arg His Lys Ser Asn Ala Pro Asp Ala Cys Phe Phe Phe Ala Asp Asn  
 565 570 575

Val Val Ala Ile Asp His Gln Leu Asp Asp Val Tyr Ile Leu Ser Leu  
 580 585 590

Tyr Glu Glu Gly Thr Ala Glu Thr Ser Phe Leu Asn Asp Thr Glu Glu  
 595 600 605

Lys Leu Ile Ser Leu Met Gly Leu Ser Thr Arg Lys Leu Glu Asp Gln  
 610 615 620

Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro  
 625 630 635 640

Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys  
 645 650 655

Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn  
 660 665 670

Arg Arg Lys Ile Gly Asn Ala Asp Pro Leu Gly Leu Tyr Leu His Leu  
 675 680 685



Arg Glu Arg Asn Pro Ala Pro Tyr Ala Ala Phe Leu Asn Phe Ser Asn  
690 695 700

Ala Asn Leu Ser Leu Cys Ser Ser Ser Pro Glu Arg Phe Leu Lys Leu  
705 710 715 720

Asp Arg Asn Gly Met Leu Glu Ala Lys Pro Ile Lys Gly Thr Ile Ala  
725 730 735

Arg Gly Ser Thr Pro Glu Glu Asp Glu Phe Leu Lys Leu Gln Leu Lys  
740 745 750

Leu Ser Glu Lys Asn Gln Ala Glu Asn Leu Met Ile Val Asp Leu Leu  
755 760 765

Arg Asn Asp Leu Gly Arg Val Cys Glu Pro Gly Ser Val His Val Pro  
770 775 780

Asn Leu Met Asp Val Glu Ser Tyr Thr Thr Val His Thr Met Val Ser  
785 790 795 800

Thr Ile Arg Gly Leu Lys Lys Thr Asp Ile Ser Pro Val Glu Cys Val  
805 810 815

Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly Ala Pro Lys Leu Arg  
820 825 830

Ser Val Glu Ile Leu Asp Ser Leu Glu Asn Cys Ser Arg Gly Leu Tyr  
835 840 845

Ser Gly Ser Ile Gly Tyr Phe Ser Tyr Asn Gly Thr Phe Asp Leu Asn  
850 855 860

Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly  
865 870 875 880

Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu  
885 890 895

Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe  
900 905 910

Cys Ser Asp Gln Arg Arg Gln  
915

&lt;210&gt; 77

&lt;211&gt; 1329

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1329)

&lt;223&gt; 58351A

&lt;400&gt; 77

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Met Gly Asp Ser Gly Lys Leu Glu Ala Thr Ile Asp Arg Leu Leu Asn	
1 5 10 15	
gaa gag aag cag atg aga ctc gcc gaa aac gta gcc ggt aca agg aaa	96
Glu Glu Lys Gln Met Arg Leu Ala Glu Asn Val Ala Gly Thr Arg Lys	
20 25 30	
gcc gcc act gag att ctt cag ctt tgt ttc gat gct aag gat tgg aaa	144
Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys	
35 40 45	
ctt ctg aat gag cag att ctc aat ctc tct aag aaa cgt ggt cag ctc	192
Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu	
50 55 60	
aaa cag gct gtg caa tcc atg gtg cag caa gca atg cag tat atc gat	240
Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp	
65 70 75 80	
cag aca cca gac att gaa act cgg ata gag ctt atc aag acg ctg aac	288
Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn	
85 90 95	
aat gta tct gct gga aag ata tat gtt gaa atc gag agg gca cgt ctc	336
Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu	
100 105 110	
acc aag aaa ctt gct aag att aag gaa gaa cag ggt cag ata gct gaa	384
Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu	
115 120 125	
gct gca gat ctt atg caa gaa gtt gct gtg gag aca ttt ggt gct atg	432
Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met	
130 135 140	
gca aaa act gag aaa att gca ttt atc ctt gaa caa gtt cgc ttg tgc	480

Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys	
145 150 155 160	
ttg gat cgt caa gat ttt gtt cgt gca caa atc tta tct agg aag atc	528
Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile	
165 170 175	
aat cct aga gtt ttt gac gca gat'aca aaa aaa gat aag aag aaa cct	576
Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Lys Pro	
180 185 190	
aag gaa ggt gat aac atg gta gaa gag gct cct gct gat ata cca acc	624
Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr	
195 200 205	
ctt ttg gag ctt aag cga att tac tac gag ctt atg att cgg tac tat	672
Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr	
210 215 220	
tct cat aac aat gag tac att gaa atc tgc cgt agc tac aag gcg ata	720
Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile	
225 230 235 240	
tat gat atc cct tca gta aaa gaa act ccg gag cag tgg att ccg gtc	768
Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val	
245 250 255	
ctg agg aag atc tgc tgg ttc ttg gtc ttg gca cct cat gac cca atg	816
Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met	
260 265 270	
caa tca agc ttg ctc aat gca act ctg gaa gac aag aat tta tca gaa	864
Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu	
275 280 285	
atc cct gat ttc aag atg ctt cta aaa cag gta gtg aca atg gag gtt	912
Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val	
290 295 300	
att caa tgg aca tct ctg tgg aac aaa tac aag gat gag ttc gag aaa	960
Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys	
305 310 315 320	
gag aaa agc atg att gga ggt tct ttg ggt gac aaa gct ggt gaa gat	1008
Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp	
325 330 335	
ctg aaa ctg aga atc atc gaa cat aat atc ctc gtt gtc tca aag tac	1056
Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr	
340 345 350	
tac gca agg ata acc tta aag aga ctt gcc gag ctt tta tgc ctg agc	1104
Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser	
355 360 365	
atg gag gag gcg gag aag cat cta tcg gag atg gta gtg tca aaa gca	1152
Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala	
370 375 380	
ctg att gca aaa ata gac aga cca tct gga att gtg tgc ttc cag atc	1200

Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile  
 385 390 395 400  
 gca aag gac agc aac gag att cta aac tcg tgg gca ggg aat ttg gag 1248  
 Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu  
 405 410 415  
 aag ctt cta gat ctt gtg gaa aag agt tgc cac caa att cac aag gaa 1296  
 Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu  
 420 425 430  
 acc atg gtt cac aaa gcc gct ctc aga cct tga 1329  
 Thr Met Val His Lys Ala Ala Leu Arg Pro  
 435 440

<210> 78

<211> 442

<212> PRT

<213> Arabidopsis thaliana

<400> 78

Met Gly Asp Ser Gly Lys Leu Glu Ala Thr Ile Asp Arg Leu Leu Asn  
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 20 25 30

Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys  
 35 40 45

Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu  
 50 55 60

Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp  
 65 70 75 80

Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn  
 85 90 95

Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu  
 100 105 110

Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu  
 115 120 125

Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met  
 130 135 140

Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys  
 145 150 155 160

Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile  
 165 170 175

Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Lys Pro  
 180 185 190

Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr  
 195 200 205

Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr  
 210 215 220

Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile  
 225 230 235 240

Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val  
 245 250 255

Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met  
 260 265 270

Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu  
 275 280 285

Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val  
 290 295 300

Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys  
 305 310 315 320

Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp  
 325 330 335

Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr  
 340 345 350

Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser  
 355 360 365

Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala  
 370 375 380

Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile  
 385 390 395 400

Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu  
 405 410 415

Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu  
 420 425 430

Thr Met Val His Lys Ala Ala Leu Arg Pro  
 435 440

<210> 79

<211> 435

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(435)

<223> 60944

<400> 79  
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 1 5 10 15  
 cct tct ctg caa tta aga aag ccg gtg atg gcg gca gtg aaa gga gga 96  
 Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly  
 20 25 30  
 aaa caa tcg gtg aga aga agc agc aat acg gtg gtt cag ata acg tgt 144  
 Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys  
 35 40 45  
 cgt aag aag gaa ttg cat cct gaa ttc cac gaa gac gca aag gtt tac 192  
 Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr  
 50 55 60  
 tgc aat gga gag ctg gtg atg act aca gga gga aca aag aaa gag tat 240  
 Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr  
 65 70 75 80

gtg gtt gat gta tgg tca ggt aac cat ccg ttt tac ctc ggg aat cgt 288  
Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg  
85 90 95

tcg gct ttg atg gtt gat gct gat caa gtt gag aag ttt cgt aag agg 336  
Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg  
100 105 110

ttc gct ggg ctt tct gag att atg gag att cct gtg ctt aaa gga gaa 384  
Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu  
115 120 125

atc att atg cct act aag aaa agt aaa ggt ccc aaa ggg aag aag aaa 432  
Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys  
130 135 140

tga 435

&lt;210&gt; 80

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 80

Met Ala Val Ser Leu Pro Asn Ser Phe Leu Gln Ile Ser Pro Cys Val  
1 5 10 15

Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly  
20 25 30

Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys  
35 40 45

Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr  
50 55 60

Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr  
65 70 75 80

Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg  
85 90 95

Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg  
100 105 110

Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu  
 115 120 125

Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys  
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<211> 2859

<212> DNA

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<222> (1) .. (2859)

<223> 62837

<400> 81

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1 5 10 15	
agg cat gtg cag gcc aaa gaa tac agg gaa cca aga ggg tgt gtg atg	96
Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met	
20 25 30	
aag atg agc agt tta aaa gca cct gtt ctg aga att cag gcc aca gaa	144
Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu	
35 40 45	
tac aga gaa cca aga ggg cgt gtg aag atg atg tcc agt tta caa gca	192
Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala	
50 55 60	
cct ctt ctg aca att cag agc ttc tca ggg tta agg gcc ccc agt gca	240
Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala	
65 70 75 80	
tta gat tat ttg gga agg cct agt cca ggt ttc ctt gtt aag tat aaa	288
Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys	
85 90 95	
ctt gca aaa tca tct ggg aga gaa aaa gct agc cga tgt gta ccc aaa	336
Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys	
100 105 110	
gca atg ttt gag cgt ttt acc gag aaa gca att aag gtc ata atg ctg	384
Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu	
115 120 125	



tct caa gag gaa gct cgg aga ctt ggc cat aac ttt gtt ggg act gag Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu 130 135 140	432
caa ata ctg ttg ggt cta att gga gaa ggg act ggg att gcc gcc aag Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys 145 150 155 160	480
gtt ctt aaa tcc atg ggg atc aat ctt aaa gat tca cgc gtg gaa gta Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val 165 170 175	528
gaa aag ata att ggg aga ggc agt gga ttc gtg gca gtg gag att cca Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro 180 185 190	576
ttt act cct cgc gca aag cgg gtg ctg gag ttg tca cta gag gaa gct Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala 195 200 205	624
cga caa ctt ggg cat aac tac att ggt tca gag cac ctt ttg ctt ggt Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly 210 215 220	672
cta ctt cgt gaa ggg gag ggt gtg gca gct cgt gtc ttg gag aat ttg Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu 225 230 235 240	720
ggg gca gat cct agt aat ata cgg aca cag gtt ata cgt atg gtc ggg Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly 245 250 255	768
gaa aac aat gaa gtc aca gca agc gtt ggt ggg gga agc agc gga aac Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Gly Ser Ser Gly Asn 260 265 270	816
agc aaa atg cca aca ctt gaa gag tat ggg act aac tta act aaa cta Ser Lys Met Pro Thr Leu Glu Glu Tyr Gly Thr Asn Leu Thr Lys Leu 275 280 285	864
gca gag gag ggt aaa ctg gat ccg gtt gtt gga agg cag cca cag atc Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile 290 295 300	912
gaa cga atg gtc cag atc ttg gct cga aga acc aag aac aac cca tgt Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys 305 310 315 320	960
ctt att gga gaa cct gga gtt ggt aag acg gca ata gca gaa gga ctt Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu 325 330 335	1008
gca cag cga ata gct agt ggt gat gtt cct gaa aca atc gag ggg aag Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys 340 345 350	1056
acg gtt ata acc ctt gat atg ggt ctt cta gtg gct gga acg aaa tac Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr 355 360 365	1104

cgt gga gag ttc gag gaa aga ttg aag aag ctt atg gag gaa atc agg Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg 370 375 380	1152
caa agt gat gag ata att ctg ttt att gat gaa gtg cac acg ctc atc Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile 385 390 395 400	1200
ggt gca gga gcc gct gaa ggt gcg atc gat gct gct aac atc tta aag Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys 405 410 415	1248
cca gct cta gca aga ggt gaa ttg cag tgt att ggt gca aca aca att Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile 420 425 430	1296
gat gag tac agg aaa cac att gag aaa gat cct gca ttg gag aga cgg Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg 435 440 445	1344
ttc cag cct gtg aaa gta cct gaa cca act gta gaa gaa gct ata cag Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln 450 455 460	1392
att ttg caa ggt ctg cgt gag cgc tat gag atc cac cac aaa ctt cga Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg 465 470 475 480	1440
tac act gat gaa gcc ttg gtt gct gct gca caa ttg tca cat cag tac Tyr Thr Asp Glu Ala Leu Val Ala Ala Ala Gln Leu Ser His Gln Tyr 485 490 495	1488
atc agt gat cgg ttt ctt ccc gac aaa gcg att gac ttg att gat gaa Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu 500 505 510	1536
gct ggg tct cgg gtt cga cta cgc cat gct cag ctt cct gag gaa gct Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala 515 520 525	1584
aga gag ctt gaa aag caa ctc agg caa atc acc aaa gag aag aat gaa Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu 530 535 540	1632
gct gtg cga agc caa gac ttc gag atg gct ggt tct cat cgt gac cgt Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg 545 550 555 560	1680
gaa ata gag ctc aag gct gag ata gct aat gtt tta tct cga ggc aaa Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys 565 570 575	1728
gaa gtg gcc aaa gcc gag aat gaa gct gag gaa gga gga cct act gtc Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val 580 585 590	1776
aca gaa tct gac atc caa cac atc gtc gcc acc tgg aca gga atc ccg Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro 595 600 605	1824

gta gag aaa gtc tcg tct gat gaa tct agc cgt ctt ctc caa atg gag Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu 610 615 620	1872
cag acc ctt cac aca aga gtc att ggc caa gat gaa gcc gtt aaa gca Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala 625 630 635 640	1920
atc agt cgg gct atc cgc cgt gcc cgt gtt ggg ctc aaa aac cca aac Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn 645 650 655	1968
cgt cct atc gcc agt ttc atc ttc tct ggt cca act ggt gtt ggg aaa Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys 660 665 670	2016
tca gag ctt gct aag gcc ttg gct gct tac tac ttc ggt tca gaa gaa Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu 675 680 685	2064
gca atg atc cgt ctt gac atg agt gag ttc atg gaa cga cac act gtt Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val 690 695 700	2112
tcg aaa ctc atc ggt tca cct cct ggt tac gta gga tac aca gaa gga Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly 705 710 715 720	2160
ggt cag tta aca gag gcg gtt cga cgc agg ccc tac act ctt gtt ctc Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Thr Leu Val Leu 725 730 735	2208
ttt gac gaa att gag aaa gca cat ccc gat gtt ttc aac atg atg ctt Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu 740 745 750	2256
cag atc cta gaa gac ggt aga cta act gat agc aaa gga aga act gtc Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val 755 760 765	2304
gat ttc aag aac acg ctt ctg atc atg act tca aac gta ggg agc agc Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser 770 775 780	2352
gtg atc gaa aaa ggt ggt aga aga att ggg ttt gat ctt gac cac gac Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp 785 790 795 800	2400
gag aaa gac agc agt tac aac aga atc aag agc tta gtg act gag gaa Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu 805 810 815	2448
cta aaa cag tat ttc aga cca gag ttc ttg aac agg tta gat gag atg Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met 820 825 830	2496
att gtt ttc aga cag tta aca aag ctg gaa gtc aag gag att gct gat Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp 835 840 845	2544

ata atg ctt aaa gaa gtg gtg gcg aga ctt gag gtc aaa gag att gag 2592  
 Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu  
 850 855 860  
 ctt cag gtg act gag agg ttt aaa gag aga gtg gtg gat gaa gga ttc 2640  
 Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe  
 865 870 875 880  
 gac ccg agt tat ggt gcg agg cca ctt aga cgt gca ata atg agg ctt 2688  
 Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu  
 885 890 895  
 ttg gag gat agt atg gcg gag aag atg ctt tca agg gac att aaa gaa 2736  
 Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu  
 900 905 910  
 gga gat tct gtg att gtt gat gtt gat gcc gaa gga agt gtg gtt gtg 2784  
 Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val  
 915 920 925  
 ttg agt ggt acc act gga cgt gtt ggt ggt ttt gct gct gaa gaa gcc 2832  
 Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala  
 930 935 940  
 atg gaa gat cct att cca ata ttg tag 2859  
 Met Glu Asp Pro Ile Pro Ile Leu  
 945 950

&lt;210&gt; 82

&lt;211&gt; 952

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 82

Met Ala Trp Ser Ile Ala Leu Leu Thr Pro Pro Phe Phe Gly Pro Gly  
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Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met  
 20 25 30

Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu  
 35 40 45

Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala  
 50 55 60

Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala  
 65 70 75 80

Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys  
                                   85                                  90                                  95

Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys  
                                   100                                  105                                  110

Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu  
                                   115                                  120                                  125

Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu  
                                   130                                  135                                  140

Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys  
                                   145                                  150                                  155                                  160

Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val  
                                   165                                  170                                  175

Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro  
                                   180                                  185                                  190

Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala  
                                   195                                  200                                  205

Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly  
                                   210                                  215                                  220

Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu  
                                   225                                  230                                  235                                  240

Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly  
                                   245                                  250                                  255

Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Gly Ser Ser Gly Asn  
                                   260                                  265                                  270

Ser Lys Met Pro Thr Leu Glu Glu Tyr Gly Thr Asn Leu Thr Lys Leu  
                                   275                                  280                                  285

Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile  
                                   290                                  295                                  300

Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys  
                                   305                                  310                                  315                                  320

Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu  
 325 330 335

Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys  
 340 345 350

Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr  
 355 360 365

Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg  
 370 375 380

Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile  
 385 390 395 400

Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys  
 405 410 415

Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile  
 420 425 430

Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg  
 435 440 445

Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln  
 450 455 460

Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg  
 465 470 475 480

Tyr Thr Asp Glu Ala Leu Val Ala Ala Ala Gln Leu Ser His Gln Tyr  
 485 490 495

Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu  
 500 505 510

Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala  
 515 520 525

Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu  
 530 535 540

Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg  
 545 550 555 560

Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys  
 565 570 575

Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val  
 580 585 590

Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro  
 595 600 605

Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu  
 610 615 620

Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala  
 625 630 635 640

Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn  
 645 650 655

Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys  
 660 665 670

Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu  
 675 680 685

Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val  
 690 695 700

Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly  
 705 710 715 720

Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Thr Leu Val Leu  
 725 730 735

Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu  
 740 745 750

Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val  
 755 760 765

Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser  
 770 775 780

Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp  
 785 790 795 800

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<212>      DNA
<213>      Arabidopsis thaliana
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att atc tct tct tct acc tct act atg cag aat ttg aag gag att gca 96  
 Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala  
 20 25 30

gca ctc atc gat act ggg tct tac acg aag gag gtt cgt cgt att gct 144  
 Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala  
 35 40 45

cgt gct gtg cgt ctc act ata ggg ctt agg cag aaa ctc acc ggc tct 192  
 Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser  
 50 55 60

gtg ctc tct tcc ttc ctg gat ttt gct ttg gtt cca gga tcc gaa gct 240  
 Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala  
 65 70 75 80

cac tct cgc ctc tct tcc ttt gtt cct aag ggt gat gaa cat gac atg 288  
 His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met  
 85 90 95

gaa gtt gat act gcc tca tcg gcc aca caa gct gct cct tct aag cat 336  
 Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His  
 100 105 110

cta cct gca gag ctc gag atc tac tgc tac ttc att gtt ctt ctt ttt 384  
 Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe  
 115 120 125

ctg att gat cag aag aag tac aac gag gct aaa gct tgt tct tca gca 432  
 Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala  
 130 135 140

agc att gct cgt ctc aag aac gtc aac cga agg acc att gat gtg ata 480  
 Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile  
 145 150 155 160

gca tca aga ctc tac ttt tac tat tct ttg agt tat gag caa acc ggt 528  
 Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly  
 165 170 175

gat ctt gct gaa att cgc ggt act ctt ctt gcg ttg cat cat tct gca 576  
 Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala  
 180 185 190

acg cta aga cac gat gag ctg ggt cag gaa acc ctt ctg aac ctg ttg 624  
 Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu  
 195 200 205

cta cgt aac tat ttg cat tac aac ctc tat gat cag gca gag aag cta 672  
 Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu  
 210 215 220

aga tca aag gca cct cgc ttt gag gct cat tca aac caa cag ttt tgt 720

Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys	
225 230 235 240	
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Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr	
245 250 255	
acg gac gca aaa gag agc ctt ctt cag gcg gcc agg aaa gcc cct ata	816
Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile	
260 265 270	
gca gct ttg ggc ttc agg atc caa tgc aat aaa tgg gca att ctg gtt	864
Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val	
275 280 285	
cgt cta ctg ctg ggt gag ata cca gag cgt tct atc ttc act caa aag	912
Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys	
290 295 300	
ggt atg gag aag gcc ctc aga ccc tac ttc gag cta aca aat gcg gtt	960
Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val	
305 310 315 320	
agg att ggg gac ttg gag ttg ttt agg aca gtc cag gag aag ttc ttg	1008
Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu	
325 330 335	
gac aca ttt gct caa gac aga acg cac aat ctc atc gtg cga ctc cgc	1056
Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg	
340 345 350	
cac aat gtc atc agg act gga ctg cgg aac ata agt atc tcc tac tca	1104
His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Ile Ser Tyr Ser	
355 360 365	
aga atc tct tta ccc gat gtt gcc aaa aag ctg agg ctc aac tct gaa	1152
Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu	
370 375 380	
aac cct gtg gct gat gcg gaa agc atc gtg gca aag gcc ata cgc gac	1200
Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp	
385 390 395 400	
gga gct att gat gct aca atc gat cac aaa aac gga tgc atg gtc tcc	1248
Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser	
405 410 415	
aaa gaa act ggg gac atc tac tcg acg aat gag cca caa act gcg ttc	1296
Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe	
420 425 430	
aac tca aga att gct ttc tgc ctc aac atg cat aac gaa gct gtc aga	1344
Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg	
435 440 445	
gca ttg agg ttt cct cct aac act cac aag gag aaa gaa agc gat gag	1392
Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Glu Ser Asp Glu	
450 455 460	
aag agg aga gag agg aag caa cag gaa gaa gag ctt gct aag cat atg	1440

Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met  
 465 470 475 480

gct gag gaa gac gat gat gat ttt tag  
 Ala Glu Glu Asp Asp Asp Asp Phe  
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1467

&lt;210&gt; 84

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 84

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Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala  
 20 25 30

Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala  
 35 40 45

Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser  
 50 55 60

Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala  
 65 70 75 80

His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met  
 85 90 95

Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His  
 100 105 110

Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe  
 115 120 125

Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala  
 130 135 140

Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile  
 145 150 155 160

Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly  
165 170 175

Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala  
180 185 190

Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu  
195 200 205

Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu  
210 215 220

Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys  
225 230 235 240

Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr  
245 250 255

Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile  
260 265 270

Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val  
275 280 285

Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys  
290 295 300

Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val  
305 310 315 320

Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu  
325 330 335

Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg  
340 345 350

His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Ile Ser Tyr Ser  
355 360 365

Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu  
370 375 380

Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp  
385 390 395 400

Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser  
 405 410 415

Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe  
 420 425 430

Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg  
 435 440 445

Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Glu Ser Asp Glu  
 450 455 460

Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met  
 465 470 475 480

Ala Glu Glu Asp Asp Asp Asp Phe  
 485

<210> 85

<211> 282

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (282)

<223> 68181

<400> 85  
 atg gac gca agc atg atg gct gga ctt gat ggt ctt cct gaa gaa gac 48  
 Met Asp Ala Ser Met Met Ala Gly Leu Asp Gly Leu Pro Glu Glu Asp  
 1 5 10 15

aaa gcc aaa atg gcc tcc atg atc gat cag ctt cag ctc cgt gat agt 96  
 Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser  
 20 25 30

ttg agg atg tac aat tca ttg gtg gag agg tgt ttc gtg gac tgt gtt 144  
 Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val  
 35 40 45

gat agc ttc aca cgc aaa tct ctg cag aaa caa gag gag act tgt gtg 192  
 Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val  
 50 55 60

atg cgt tgc gct gag aag ttc ctt aag cat acg atg cgt gtt ggt atg 240  
 Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met  
 65 70 75 80

cgg ttt gct gag ctc aat cag aac gca cca acc caa gac tga 282  
 Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp  
 85 90

<210> 86

<211> 93

<212> PRT

<213> Arabidopsis thaliana

<400> 86

Met Asp Ala Ser Met Met Ala Gly Leu Asp Gly Leu Pro Glu Glu Asp  
 1 5 10 15

Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser  
 20 25 30

Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val  
 35 40 45

Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val  
 50 55 60

Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met  
 65 70 75 80

Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp  
 85 90

<210> 87

<211> 816

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

&lt;222&gt; (1) .. (816)

&lt;223&gt; 70913

&lt;400&gt; 87

atg caa tca aaa ccg gga aga gaa aac gaa gag gaa gtc aat aat cac	48
Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His	
1 5 10 15	
cat gct gtt cag cag ccg atg atg tat gca gag ccc tgg tgg aaa aac	96
His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn	
20 25 30	
aac tcc ttt ggt gtt gta cct caa gcg aga cct tct gga att cca tca	144
Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser	
35 40 45	
aat tcc tct tct ttg gat tgc ccc aat ggt tcc gag tca aac gat gtt	192
Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val	
50 55 60	
cat tca gca tct gaa gac ggt gcg ttg aat ggt gaa aac gat ggc act	240
His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr	
65 70 75 80	
tgg aag gat tca caa gct gca act tcc tct cgt tca gat aat cac gga	288
Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly	
85 90 95	
atg gaa gga aat gac cca gcg ctc tct atc cgt aac atg cat gat cag	336
Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln	
100 105 110	
cca ctt gta caa cca cca gag ctt gtt gga cac tat atc gct tgt gtc	384
Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val	
115 120 125	
cca aac cca tat cag gat cca tat tat ggg gga ttg atg gga gca tat	432
Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr	
130 135 140	
ggt cat cag caa ttg ggt ttt cgt cca tat ctt gga atg cct cgt gaa	480
Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu	
145 150 155 160	
aga aca gct ctg cca ctt gac atg gca caa gag ccc gtt tat gtg aat	528
Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn	
165 170 175	
gca aag cag tac gag gga att cta agg cga aga aaa gca cgt gcc aag	576
Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys	
180 185 190	
gca gag cta gag agg aaa gtc atc cgg gac aga aag cca tat ctt cac	624
Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His	
195 200 205	
gag tca aga cac aag cat gca atg aga agg gca cga gcg agt gga ggc	672

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly  
 210 215 220  
 cgg ttt gcg aag aaa agt gag gta gaa gcg gga gag gat gca gga ggg 720  
 Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly  
 225 230 235 240  
 aga gac aga gaa agg ggt tca gca acc aac tca tca ggc tct gaa caa 768  
 Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln  
 245 250 255  
 gtt gag aca gac tct aat gag acc ctg aat tct tct ggt gca cca taa 816  
 Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro  
 260 265 270

<210> 88

<211> 271

<212> PRT

<213> Arabidopsis thaliana

<400> 88

Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His  
 1 5 10 15

His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn  
 20 25 30

Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser  
 35 40 45

Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val  
 50 55 60

His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr  
 65 70 75 80

Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly  
 85 90 95

Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln  
 100 105 110

Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val  
 115 120 125



Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr  
 130 135 140

Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu  
 145 150 155 160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn  
 165 170 175

Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys  
 180 185 190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His  
 195 200 205

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly  
 210 215 220

Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly  
 225 230 235 240

Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln  
 245 250 255

Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro  
 260 265 270

<210> 89

<211> 990

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1) .. (990)

<223> 71067

<400> 89

atg agt cgc cgg gtg gaa tac acg tta gct cct ccg cag agg aat gaa  
 Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu  
 1 5 10 15

48

tct gac ggt ttt gat tat ccc gac ggt atc cca ata tca tac aat ctt Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu 20 25 30	96
cat agg ctt cgt cac ttt gag tgt gaa ggc agt tat ccc aag tat cct His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro 35 40 45	144
tat ggt tct ttg gtc aag ttt tat gca atg gtg gga ctt cat cgt tac Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr 50 55 60	192
aat gtg ttg gag ggg aaa aat ttg cag ctc gat acc cta aag agt ttc Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe 65 70 75 80	240
aac atg aga atc aat tgt ggt gct tct tct tac tac att act ttg gct Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala 85 90 95	288
gca cgc gtt cca gat agc ggt ttg aag cag atc ttt cag gtt cta gtt Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val 100 105 110	336
cat gaa gag cgt ctt ggc agt tta gac atg aca tgt act atc gct aga His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg 115 120 125	384
cct cga gtg act acc aat gtg cct ttt cta cgt ccg cac agc gaa tca Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser 130 135 140	432
gag tat gat tat atg gac aat gat gaa ttg cct gac tgg cct tca gag Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu 145 150 155 160	480
att gct ttc gat gat aca aaa cgg ttt cat ctg gtg aag gaa tca gag Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu 165 170 175	528
ttg cga gac aat gat tgg att cga ctc tat ttg gaa ctt aca ctt gtt Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val 180 185 190	576
gct cac gat agg ttt ctt aca gtt cac tat ctc tcc cag ttg gag att Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile 195 200 205	624
gtg aaa gtt gcg att gaa gaa gtg gag caa ccg aat gcg agt ctc aac Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn 210 215 220	672
acc aaa act aca ttt gtc tac ata act tat aag gac ttg gca aag gct Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala 225 230 235 240	720
cag att ggt gag ccg gtt gat cgc aaa gct att gtt aga aaa atc atc Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile 245 250 255	768

aat gag act acg gga ctc ttg aga ctc cgg ggt gat tat tgg agt gga 816  
 Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly  
 260 265 270  
 gaa aga agt gtg atc act ccg gag gag gaa tat atg ctt ctc cat ggc 864  
 Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly  
 275 280 285  
 gga gaa aaa gtt cga aac aat gag cag cgt tct aaa aaa ctt aag cgt 912  
 Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg  
 290 295 300  
 cgt gta ggt gtt cat agg cta tgg cga tgg tgg tac cag gct tac aaa 960  
 Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys  
 305 310 315 320  
 aac cgt ggc ctc cgc tcg tcg tct tat taa 990  
 Asn Arg Gly Leu Arg Ser Ser Ser Tyr  
 325

&lt;210&gt; 90

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 90

Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu  
 1 5 10 15  
 Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu  
 20 25 30  
 His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro  
 35 40 45  
 Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr  
 50 55 60  
 Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe  
 65 70 75 80  
 Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala  
 85 90 95  
 Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val  
 100 105 110

His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg  
 115 120 125

Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser  
 130 135 140

Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu  
 145 150 155 160

Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu  
 165 170 175

Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val  
 180 185 190

Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile  
 195 200 205

Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn  
 210 215 220

Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala  
 225 230 235 240

Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile  
 245 250 255

Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly  
 260 265 270

Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly  
 275 280 285

Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg  
 290 295 300

Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys  
 305 310 315 320

Asn Arg Gly Leu Arg Ser Ser Ser Tyr  
 325

&lt;210&gt; 91

&lt;211&gt; 1614

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1614)

&lt;223&gt; 71654

&lt;400&gt; 91

atg gcg ctc gtg aaa acg gaa acg cag gcg tta gga aac cac cag cat	48
Met Ala Leu Val Lys Thr Glu Thr Gln Ala Leu Gly Asn His Gln His	
1 5 10 15	
tct tca agg ttt ggt tgc ctt tac gtc ggt gat ctt agc cca gac gtg	96
Ser Ser Arg Phe Gly Ser Leu Tyr Val Gly Asp Leu Ser Pro Asp Val	
20 25 30	
acg gag aaa gat ctc att gat aag ttc tct ttg aat gtt ccg gta gtg	144
Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val	
35 40 45	
tcc gtt cat ctt tgc cgt aac tct gtc acc gga aaa tcc atg tgt tac	192
Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr	
50 55 60	
gct tac atc aac ttc gat tca cct ttc agc gca tgc aat gct atg act	240
Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr	
65 70 75 80	
cgc tta aac cat agt gat ttg aag gga aag gct atg cga ata atg tgg	288
Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp	
85 90 95	
tct cag agg gat ctt gcg tac cgt cgt cgt act cgt act ggt ttt gca	336
Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala	
100 105 110	
aat cta tac gta aag aat ctg gat agc tgc att act agc agt tgc tta	384
Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu	
115 120 125	
gag cga atg ttt tgc ccc ttt ggt tcc ata ctt tct tgc aaa gtc gtt	432
Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val	
130 135 140	
gaa gag aat ggc caa agt aaa ggt ttt ggc ttt gtt cag ttt gat aca	480
Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr	
145 150 155 160	
gag caa tct gct gta tct gct cgt tct gct ctc cac ggc tct atg gtt	528

Glu Gln Ser Ala Val Ser Ala Arg Ser Ala Leu His Gly Ser Met Val	
165	170 175
tat ggc aag aaa ctg ttt gtt gcc aag ttc atc aac aag gat gaa aga	576
Tyr Gly Lys Lys Leu Phe Val Ala Lys Phe Ile Asn Lys Asp Glu Arg	
180	185 190
gca gct atg gca gga aat caa gac tct aca aac gtt tat gtg aag aat	624
Ala Ala Met Ala Gly Asn Gln Asp Ser Thr Asn Val Tyr Val Lys Asn	
195	200 205
ctg atc gaa act gtt aca gat gat tgt cta cat aca ctg ttt tct caa	672
Leu Ile Glu Thr Val Thr Asp Asp Cys Leu His Thr Leu Phe Ser Gln	
210	215 220
tat gga act gtc tct agt gtt gtg gtt atg agg gat ggt atg gga aga	720
Tyr Gly Thr Val Ser Ser Val Val Val Met Arg Asp Gly Met Gly Arg	
225	230 235 240
tct aga ggt ttc gga ttt gtt aac ttc tgc aat cca gaa aat gct aag	768
Ser Arg Gly Phe Gly Phe Val Asn Phe Cys Asn Pro Glu Asn Ala Lys	
245	250 255
aaa gct atg gaa tct ctc tgt gga cta caa ctt gga tcg aag aaa ttg	816
Lys Ala Met Glu Ser Leu Cys Gly Leu Gln Leu Gly Ser Lys Lys Leu	
260	265 270
ttt gtt ggt aag gca ctc aag aaa gat gaa agg agg gag atg ctg aaa	864
Phe Val Gly Lys Ala Leu Lys Lys Asp Glu Arg Arg Glu Met Leu Lys	
275	280 285
cag aaa ttc agt gac aac ttt att gca aag cct aac atg aga tgg tcc	912
Gln Lys Phe Ser Asp Asn Phe Ile Ala Lys Pro Asn Met Arg Trp Ser	
290	295 300
aat ctg tac gtg aag aac ttg agt gaa tca atg aat gaa aca aga ctg	960
Asn Leu Tyr Val Lys Asn Leu Ser Glu Ser Met Asn Glu Thr Arg Leu	
305	310 315 320
cga gaa atc ttt gga tgc tat ggg caa ata gtt tca gct aaa gtg atg	1008
Arg Glu Ile Phe Gly Cys Tyr Gly Gln Ile Val Ser Ala Lys Val Met	
325	330 335
tgt cat gag aat ggc aga agt aaa gga ttc ggc ttt gtg tgc ttc tct	1056
Cys His Glu Asn Gly Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser	
340	345 350
aac tgt gaa gag tcc aaa cag gct aaa aga tat ctc aat ggg ttc tta	1104
Asn Cys Glu Glu Ser Lys Gln Ala Lys Arg Tyr Leu Asn Gly Phe Leu	
355	360 365
gtt gat gga aag cca ata gtt gtt cga gtt gca gag cgc aaa gag gat	1152
Val Asp Gly Lys Pro Ile Val Val Arg Val Ala Glu Arg Lys Glu Asp	
370	375 380
cga atc aag agg ttg cag caa tat ttt cag gca cag cca cgc cag tac	1200
Arg Ile Lys Arg Leu Gln Gln Tyr Phe Gln Ala Gln Pro Arg Gln Tyr	
385	390 395 400
acg caa gct cct tct gcc cct tca cca gct cag cca gtc ctc tca tat	1248

Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr  
405 410 415

gtg tcc agc tca tat ggt tgc ttt cag cca ttc cag gtc ggg aca tct 1296  
Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser  
420 425 430

tat tac tat atg ggc aat cag gtg cca caa atg tcc ggt cac caa aac 1344  
Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn  
435 440 445

atc acc acc tac gtt cca gct ggg aaa gtg cct ctc aag gag aga aga 1392  
Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg  
450 455 460

tca atg cat ctg gtc tac aaa cat ccg gct tat ccc gtt gcc aag agg 1440  
Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg  
465 470 475 480

ggt gct aaa cag aca ctg gtt ttt aag ggt gag gtt aac aga aat tta 1488  
Gly Ala Lys Gln Thr Leu Val Phe Lys Gly Glu Val Asn Arg Asn Leu  
485 490 495

gag gct gca aca tgc tcc aaa gca aca aca tct gag gag aac cgt aaa 1536  
Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys  
500 505 510

gaa gaa cga aga ttg act ttg tca gga aag ttg tca cca gaa gtg aag 1584  
Glu Glu Arg Arg Leu Thr Leu Ser Gly Lys Leu Ser Pro Glu Val Lys  
515 520 525

gta gag gaa tca gga aaa caa ttg caa tga 1614  
Val Glu Glu Ser Gly Lys Gln Leu Gln  
530 535

&lt;210&gt; 92

&lt;211&gt; 537

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 92

Met Ala Leu Val Lys Thr Glu Thr Gln Ala Leu Gly Asn His Gln His  
1 5 10 15

Ser Ser Arg Phe Gly Ser Leu Tyr Val Gly Asp Leu Ser Pro Asp Val  
20 25 30

Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val  
35 40 45

Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr  
 50 55 60

Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr  
 65 70 75 80

Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp  
 85 90 95

Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala  
 100 105 110

Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu  
 115 120 125

Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val  
 130 135 140

Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr  
 145 150 155 160

Glu Gln Ser Ala Val Ser Ala Arg Ser Ala Leu His Gly Ser Met Val  
 165 170 175

Tyr Gly Lys Lys Leu Phe Val Ala Lys Phe Ile Asn Lys Asp Glu Arg  
 180 185 190

Ala Ala Met Ala Gly Asn Gln Asp Ser Thr Asn Val Tyr Val Lys Asn  
 195 200 205

Leu Ile Glu Thr Val Thr Asp Asp Cys Leu His Thr Leu Phe Ser Gln  
 210 215 220

Tyr Gly Thr Val Ser Ser Val Val Val Met Arg Asp Gly Met Gly Arg  
 225 230 235 240

Ser Arg Gly Phe Gly Phe Val Asn Phe Cys Asn Pro Glu Asn Ala Lys  
 245 250 255

Lys Ala Met Glu Ser Leu Cys Gly Leu Gln Leu Gly Ser Lys Lys Leu  
 260 265 270

Phe Val Gly Lys Ala Leu Lys Lys Asp Glu Arg Arg Glu Met Leu Lys  
 275 280 285



Gln Lys Phe Ser Asp Asn Phe Ile Ala Lys Pro Asn Met Arg Trp Ser  
 290 295 300

Asn Leu Tyr Val Lys Asn Leu Ser Glu Ser Met Asn Glu Thr Arg Leu  
 305 310 315 320

Arg Glu Ile Phe Gly Cys Tyr Gly Gln Ile Val Ser Ala Lys Val Met  
 325 330 335

Cys His Glu Asn Gly Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser  
 340 345 350

Asn Cys Glu Glu Ser Lys Gln Ala Lys Arg Tyr Leu Asn Gly Phe Leu  
 355 360 365

Val Asp Gly Lys Pro Ile Val Val Arg Val Ala Glu Arg Lys Glu Asp  
 370 375 380

Arg Ile Lys Arg Leu Gln Gln Tyr Phe Gln Ala Gln Pro Arg Gln Tyr  
 385 390 395 400

Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr  
 405 410 415

Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser  
 420 425 430

Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn  
 435 440 445

Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg  
 450 455 460

Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg  
 465 470 475 480

Gly Ala Lys Gln Thr Leu Val Phe Lys Gly Glu Val Asn Arg Asn Leu  
 485 490 495

Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys  
 500 505 510

Glu Glu Arg Arg Leu Thr Leu Ser Gly Lys Leu Ser Pro Glu Val Lys  
 515 520 525

Val Glu Glu Ser Gly Lys Gln Leu Gln  
530 535

<210> 93

<211> 657

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(657)

<223> ET3172

<400> 93  
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gaa gaa caa cac tat tct tta tca aga ctc tcc gtt tgt tcc aac tac 96  
Glu Glu Gln His Tyr Ser Leu Ser Arg Leu Ser Val Cys Ser Asn Tyr  
20 25 30  
gac ggc gat gaa gcc gac ggt gag tct tct gct tcc gac gag aaa cgt 144  
Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg  
35 40 45  
gtt gtc cac ggc gga gga gag aaa tcc atg gag gag cta aat ttt tca 192  
Val Val His Gly Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser  
50 55 60  
gat tct gat aaa gaa tca acc ggt tgt caa tct ctc ccg gcg aca cct 240  
Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro  
65 70 75 80  
ccg aga cgg aga cgg cgg aga ggc ggt gga gga gga gga tat tta gcg 288  
Pro Arg Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Tyr Leu Ala  
85 90 95  
gtg agt tct ccg gtt tcc ggc gat aaa gct tac gct agc gag aac gaa 336  
Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu  
100 105 110  
gta caa aag acg aat aac aat cag agg aga agg agg aga ttg aaa ccg 384  
Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro  
115 120 125  
gag tgt cca ccg tgg gtt gat agt atg cgg agg agc tac gtc gga gat 432  
Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp  
130 135 140

gaa cag agt agt cac ggt ggt tac gga gga gga gtg gtg gtt gtt acg 480  
 Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Gly Val Val Val Val Thr  
 145 150 155 160  
 agg cct ata gga gga gga agg cca ttg tgt atg gat tta gaa gaa gtc 528  
 Arg Pro Ile Gly Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val  
 165 170 175  
 aaa gct tgt aaa gat ttg ggg ttt gag ctt gaa ccg ggt cgg gtt tcg 576  
 Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser  
 180 185 190  
 tat tcc ggg tca acg gtg gat act agt agt ggc ggc aat tct cct atc 624  
 Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile  
 195 200 205  
 tct tct aac cac cgt att tcg agt ccc ggt tag 657  
 Ser Ser Asn His Arg Ile Ser Ser Pro Gly  
 210 215

&lt;210&gt; 94

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 94

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 Glu Glu Gln His Tyr Ser Leu Ser Arg Leu Ser Val Cys Ser Asn Tyr  
 20 25 30  
 Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg  
 35 40 45  
 Val Val His Gly Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser  
 50 55 60  
 Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro  
 65 70 75 80  
 Pro Arg Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Tyr Leu Ala  
 85 90 95  
 Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu  
 100 105 110

Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro  
 115 120 125

Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp  
 130 135 140

Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Gly Val Val Val Val Thr  
 145 150 155 160

Arg Pro Ile Gly Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val  
 165 170 175

Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser  
 180 185 190

Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile  
 195 200 205

Ser Ser Asn His Arg Ile Ser Ser Pro Gly  
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gtc tac aaa aat gct att ttc atg tgc gag cgt ctc tgc gct gag ttt 96  
 Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe  
 20 25 30

cct tct gag gtt aat ttg cag cta tta gcc acc agc tac ctg cag aat 144

Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Thr Ser Tyr Leu Gln Asn  
 35 40 45  
 aat caa gct tac agt gca tat cat ctg cta aag gga aca caa atg gct 192  
 Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala  
 50 55 60  
 cag tcc cga tac ttg ttc gca tta tca tgc ttc cag atg gac ctt ctc 240  
 Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu  
 65 70 75 80  
 aat gaa gct gaa tct gca ctc tgc cct gtt aat gaa cct ggt gcg gag 288  
 Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu  
 85 90 95  
 atc cca aat ggt gca gca ggc cat tac ctt ctt gga ctt att tac aag 336  
 Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys  
 100 105 110  
 aag aat gct gct caa caa ttt aaa cag tcc ttg aca ata gac cct cta 384  
 Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu  
 115 120 125  
 ctt tgg gct gca tat gag gaa tta tgt ata tta ggt gct gct gag gaa 432  
 Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu  
 130 135 140  
 gca act gca gtt ttt ggt gaa aca gct gct ctc tcc att caa aag cag 480  
 Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln  
 145 150 155 160  
 tat atg caa caa ctg tca act tcc ctc ggc tta aac act tac aac gag 528  
 Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu  
 165 170 175  
 gaa cgt aat tca act tct act aaa aac acg agt tct gaa gat tat agt 576  
 Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser  
 180 185 190  
 cca agg cag tct aaa cac aca caa agc cat ggc ctt aaa gat atc tcc 624  
 Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser  
 195 200 205  
 gga aat ttc cat tct cat gga gtt aat gga ggt gtt tcg aac atg tca 672  
 Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser  
 210 215 220  
 ttc tat aat acg cct tcg cca gtg gct gca cag cta tcc ggt ata gct 720  
 Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala  
 225 230 235 240  
 cca cca cca ctt ttc cgg aat ttt cag cca gct gtt gca aac cca aac 768  
 Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn  
 245 250 255  
 tcc ctt att act gac agt tct cca aag tcc act gtt aac tct act ctt 816  
 Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu  
 260 265 270  
 caa gca cct aga aga aag ttt gta gat gaa gga aag tta cgt aag att 864

Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile	
275 280 285	
tct ggc aga cta ttt tct gat tct ggt cca cga cgg agt tca aga ctg	912
Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu	
290 295 300	
tct gct gat tca ggg gca aac att aat tca agt gtt gca aca gta agc	960
Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser	
305 310 315 320	
gga aat gtg aac aac gct tcc aag tat ttg gga ggt tct aaa ttg agt	1008
Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Gly Ser Lys Leu Ser	
325 330 335	
tct ttg gca ctt cgt tct gta aca ctt cgg aag gga cac tcc tgg gca	1056
Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala	
340 345 350	
aat gaa aac atg gat gaa ggg gtc cgt ggg gaa cct ttt gat gat tca	1104
Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser	
355 360 365	
agg cct aat act gcc tca acg act ggt tct atg gct tcc aat gat caa	1152
Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln	
370 375 380	
gaa gac gaa aca atg tcg att ggt ggc ata gca atg agt tct caa aca	1200
Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr	
385 390 395 400	
atc aca att ggt gtt tcg gaa att tta aac ctc ctt agg aca ctc gga	1248
Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly	
405 410 415	
gaa ggg tgt aga ctt tca tac atg tac agg tgt cag gag gca ctg gat	1296
Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp	
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acg tat atg aaa ctt cca cat aag cat tat aat aca gga tgg gtt ctt	1344
Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu	
435 440 445	
tcc cag gtc ggg aaa gca tac ttt gaa cta att gac tat tta gag gct	1392
Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala	
450 455 460	
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Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu	
465 470 475 480	
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Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met	
485 490 495	
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Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala	
500 505 510	
cct caa tct tgg tgt gct atg gga aat tgc tat agc ttg caa aag gac	1584

Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp	
515	520 525
cat gag acc gca ctg aag aat ttc cta cga gct gtt caa ctg aat cca	1632
His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro	
530	535 540
aga ttt gca tat gca cat acc tta tgt ggc cac gaa tac aca act ctt	1680
Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Thr Leu	
545	550 555 560
gag gat ttt gag aac gga atg aaa agt tac caa aac gca ctt cgt gta	1728
Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val	
565	570 575
gat aca aga cac tac aac gca tgg tac ggg ctt gga atg ata tat cta	1776
Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu	
580	585 590
cgc caa gag aag tta gag ttc tca gag cat cac ttc aga atg gct ttc	1824
Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe	
595	600 605
cta ata aac ccg agt tcc tct gtt ata atg tct tat tta ggg aca tct	1872
Leu Ile Asn Pro Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser	
610	615 620
ttg cat gcc ttg aag aga agt gag gaa gca cta gag ata atg gag caa	1920
Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln	
625	630 635 640
gcc ata gta gca gat aga aaa aac cct ctt cca atg tac cag aaa gct	1968
Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala	
645	650 655
aac ata ctt gtc tgc tta gaa aga tta gat gaa gct cta gaa gtt ctt	2016
Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu	
660	665 670
gag gag ctc aaa gag tat gcg cct tca gag agc agc gtt tac gct tta	2064
Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu	
675	680 685
atg ggc agg atc tat aag cgg cga aac atg cac gat aaa gcc atg ctt	2112
Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu	
690	695 700
cat ttc ggt cta gct tta gat atg aaa ccg cct gca act gac gtt gct	2160
His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala	
705	710 715 720
gca ata aag gct gca atg gag aaa ttg cat gtt cca gat gag atc gat	2208
Ala Ile Lys Ala Ala Met Glu Lys Leu His Val Pro Asp Glu Ile Asp	
725	730 735
gag agc ccg tga	2220
Glu Ser Pro	

&lt;210&gt; 96

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 96

Met Glu Ala Met Leu Val Asp Cys Val Asn Asn Ser Leu Arg His Phe  
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Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe  
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Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Thr Ser Tyr Leu Gln Asn  
 35 40 45

Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala  
 50 55 60

Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu  
 65 70 75 80

Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu  
 85 90 95

Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys  
 100 105 110

Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu  
 115 120 125

Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu  
 130 135 140

Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln  
 145 150 155 160

Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu  
 165 170 175

Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser  
 180 185 190



Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser  
 195 200 205

Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser  
 210 215 220

Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala  
 225 230 235 240

Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn  
 245 250 255

Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu  
 260 265 270

Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile  
 275 280 285

Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu  
 290 295 300

Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser  
 305 310 315 320

Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Gly Ser Lys Leu Ser  
 325 330 335

Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala  
 340 345 350

Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser  
 355 360 365

Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln  
 370 375 380

Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr  
 385 390 395 400

Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly  
 405 410 415

Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp  
 420 425 430

Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu  
 435 440 445

Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala  
 450 455 460

Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu  
 465 470 475 480

Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met  
 485 490 495

Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala  
 500 505 510

Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp  
 515 520 525

His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro  
 530 535 540

Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Thr Leu  
 545 550 555 560

Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val  
 565 570 575

Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu  
 580 585 590

Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe  
 595 600 605

Leu Ile Asn Pro Ser Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser  
 610 615 620

Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln  
 625 630 635 640

Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala  
 645 650 655

Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu  
 660 665 670

Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu  
675 680 685

Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu  
690 695 700

His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala  
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Glu Ser Pro

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&lt;400&gt; 100

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&lt;210&gt; 101

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; LWAD1

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(18)

&lt;223&gt; n = a, t, c, or g

&lt;400&gt; 101

ngtttgwgnat wtsgwgnt

18

&lt;210&gt; 102

&lt;211&gt; 16

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; CA50

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<210> 103

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<223> CA51

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<210> 104

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16

<210> 108

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<223> 5A

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<210> 109

<211> 30

<212> DNA

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<223> 5B

<400> 109

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30

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<223> 5C

<400> 110

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33

<210> 111

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> 3A

<400> 111

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36

<210> 112

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3B



<400> 112  
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37

<210> 113

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<213> Artificial Sequence

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<223> 3C

<400> 113  
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34

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<223> CA66

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29

<210> 115

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<223> CA67

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<223> CA68

<400> 116

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<223> JM33

<400> 117

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<210> 118

<211> 34

<212> DNA

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<223> JM34

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34

<210> 119

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> JM35

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34

<210> 120

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> QRB1

<400> 120  
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32

<210> 121

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> QRB2

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32

<210> 122

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> QRB3

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30

<210> 123

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<212> DNA

<213> Artificial Sequence

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<223> SKI1

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35

<210> 124

<211> 31

<212> DNA

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<223> SKI2

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31

<210> 125

<211> 28

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<223> SKI3

<400> 125  
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